

Access DB# 83111

# SEARCH REQUEST FORM

Scientific and Technical Information Center

CREE

Requester's Full Name: M.A. WALICKA Examiner #: 7820 Date: 11/21/02  
Art Unit: 1652 Phone Number 305-7270 Serial Number: 651786 311  
Mail Box and Bldg Room Location: 10306 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract

Title of Invention: Monitor system for measuring protein phospho #1

Inventors (please provide full names): UAGIWARA

Earliest Priority Filing Date: 09/02/1998

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO:1 Seq is OK  
SEQ ID NO:2

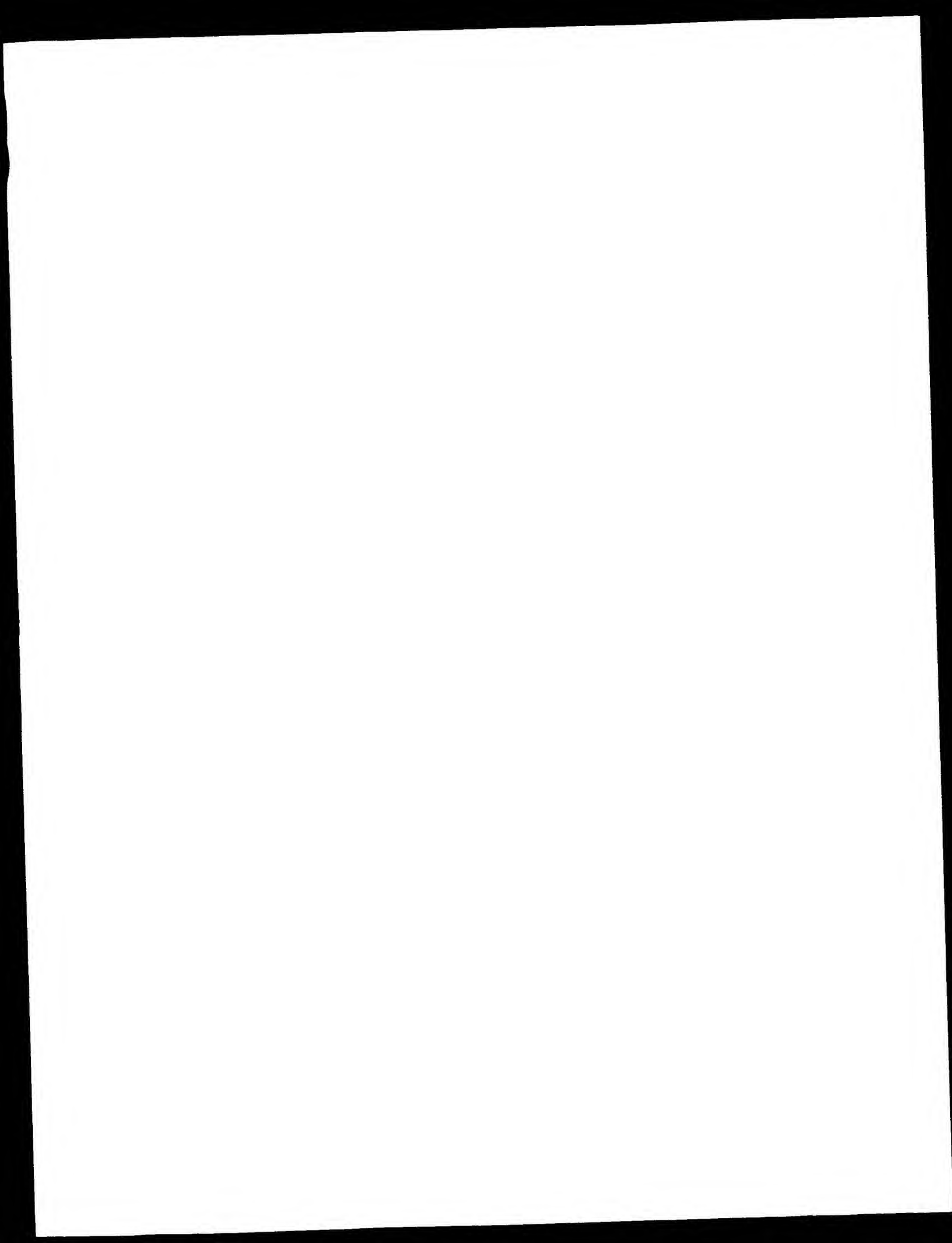
Thank you in advance.

Edward H. ...  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

Indicates

AA  
1-23  
2-23

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher	NA Sequence (#)	STN	
Searcher Phone #	AA Sequence (#)	2	Dialog
Searcher Location	Structure (#)		Questel/Orbit
Date Searcher Picked Up	Bibliographic		Dr Link
Date Completed	Litigation		Lexis/Nexis
Searcher Prep & Review Time	Fulltext		Sequence Systems
Clerical Prep Time	Patent Family		WWW Internet
Online Time	Other		Other (specify)





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DI 01-JUN-2000 (TREMBLrel. 15, last sequence update)
DI 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE cyclic AMP response element binding protein (Fragment)
OS Ovis aries (Sheep)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9949;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE PULMONARY ARTERY;
RA Dolan S., Kelly J.G., Nolan A.M.;
RT "Ovis aries cyclic AMP response element binding protein (CREB) mRNA."
RL Submitted (Aug. 1997), EMBL, GenBank, and DDBJ.
DR EMBL: AF280055; AAF90178.1; -.
DR InterPro: IPR001630; Leuzip_CREB.
DR InterPro: IPR004102; PKID.
DR Pfam: PF02173; PKID.1.
DR PRINTS: PR00041; LEUZIPPICREB.
FT NON_TER 1
FT NON_TER 231
FT NON_TER 231
SQ SEQUENCE 231 AA, 24203 MW, CF212B9587D03837 CRC64.

Query Match 83.8%; Score 93; DB 6; Length 231;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 4 EILSRPPSYRKILNDLSSD 22
IIIIIIIIIIIIIIIIIIII
DE 67 EILSRPPSYRKILNDLSSD 85

RESULT 3
P70400
ID P70400 PRELIMINARY; PRI: 257 AA.
AC P70400;
DI 01-FEB-1997 (TREMBLrel. 02, Created)
DI 01-FEB-1997 (TREMBLrel. 02, last sequence update)
DI 01-MAR-2002 (TREMBLrel. 29, last annotation update)
DE CREB (Fragment).
GN CREB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE THYMUS;
RX MEDLINE 97211815, PubMed 9058792,
RA Yang L., Ianier E.R., Kraig E.;
RT "Identification of a novel, spliced variant of CREB that is
preferentially expressed in the thymus."
RL J. Immunol. 158:2522-2525(1997).
CC - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
OC - SIMILARITY: BELONGS TO THE BZIP FAMILY.
DR EMBL: U46027; AAR64015.1; -.
DR MGD: MGI:88494; Creb1.
DR InterPro: IPR001630; Leuzip_CREB.
DR InterPro: IPR002112; Leuzip_Jun.
DR InterPro: IPR004102; PKID.
DR InterPro: IPR004827; TF_BZIP.
DR Pfam: PF00170; bZIP.1.
DR Pfam: PF02173; PKID.1.
DR PRINTS: PR00041; LEUZIPPICREB.
DR PRINTS: PR00043; LEUZIPPICJUN.
DR SMART: SM00338; BRLZ.1.
DR PROSITE: PS00036; BZIP_BASIC; 1.
KW DNA-binding; Nuclear proteins.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 257 AA, 28009 MW, 91F0RPP7711CE91FE CRC64.

Query Match 83.8%; Score 93; DB 11; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.6e-07;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPPSYRKILNDLSSD 22
IIIIIIIIIIIIIIIIIIII
DE 103 EILSRPPSYRKILNDLSSD 121

RESULT 4
Q62347
ID Q62347 PRELIMINARY; PRI: 287 AA.
AC Q62347;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DI 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Transcription factor/DNA binding protein.
GN CREB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-12901A;
RX MEDLINE 96183194, PubMed 8605979;
RA Blendsy J.A., Kaestner K.H., Schmid W., Cass P., Schutz G.;
RT "Targeting of the CREB gene leads to upregulation of a novel CREB mRNA
isoform."
RL EMBL J. 15:1098-1105(1996).
CC - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
OC - SIMILARITY: BELONGS TO THE BZIP FAMILY.
DR EMBL: X92497; CAA63242.1; -.
DR TRANSFAC: T02361; -.
DR MGD: MGI:88494; Creb1.
DR InterPro: IPR001630; Leuzip_CREB.
DR InterPro: IPR003102; PKID.
DR InterPro: IPR004827; TF_BZIP.
DR Pfam: PF00170; bZIP.1.
DR Pfam: PF02173; PKID.1.
DR PRINTS: PR00041; LEUZIPPICREB.
DR SMART: SM00338; BRLZ.1.
DR PROSITE: PS00036; BZIP_BASIC; 1.
KW DNA-binding; Nuclear proteins.
SQ SEQUENCE 287 AA, 30960 MW, 2228CR72R8991381 CRC64.

Query Match 83.8%; Score 93; DB 11; Length 287;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPPSYRKILNDLSSD 22
IIIIIIIIIIIIIIIIIIII
DE 72 EILSRPPSYRKILNDLSSD 90

RESULT 5
Q61442
ID Q61442 PRELIMINARY; PRI: 317 AA.
AC Q61442;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DI 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE C AMP responsive-element binding protein omega.
GN CREB1 OR CREB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN C CH/C-CH;
RX MEDLINE 92224899, PubMed 1532935;
RA Ruppert S., Cole T.J., Roshart M., Schmid E., Schutz G.;
RT "Multiple mRNA isoforms of the transcription activator protein CREB:
generation by alternative splicing and specific expression in primary

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SQ SEQUENCE 124 AA; 14685 MW; R2330981F7D322C9 Q9664;
Query Match 80.2%; Score 89; DB 11; Length 124;
Best local Similarity 94.7%; Pred. No. 2.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNELSSD 22
   11111111111111111111
DB 61 EILSRPSPSYRKILNELSSD 79
   11111111111111111111

RESULT 9
Q96AC7 PRELIMINARY; PRI: 137 AA.
AC Q96AC7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DI 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DI 01-MAR-2003 (TREMBlrel. 20, 33.4 aa, 3.11 aa, 1.0 aa)
DE Similar to cAMP responsive element modulator.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE: OTERUS;
RA Strausberg R.;
RL Submitted (NOV 2001) to the EMBL/GenBank/DDBJ databases
DR EMBL: BC017117; AAH17117.1;
DR InterPro: IPR003102; PKID;
DR Pfam: PF02173; PKID; 1.
SQ SEQUENCE 137 AA; 14871 MW; 6A3047664350D9P Q9C64;

Query Match 80.2%; Score 89; DB 4; Length 137;
Best local Similarity 94.7%; Pred. No. 1.5e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNELSSD 22
   11111111111111111111
DB 64 EILSRPSPSYRKILNELSSD 82
   11111111111111111111

RESULT 10
Q9D599 PRELIMINARY; PRI: 196 AA.
AC Q9D599;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DI 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DI 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Adult male testis cDNA, RIKEN full-length enriched library,
DE clone:45048A05, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi T., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gajbort T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli F., Harsh G.,
RA Blake J., Boffelli P., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nardone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenck C., Seya T., Shibata Y., Storch K.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshak Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK016156; BAB30130.1;
DE InterPro: IPR001630; leuzip_CREB.
DI InterPro: IPR002102; PKID.
DI Pfam: PF02173; PKID; 1.
DE PRINTS: PP00041; LEUZIPPCCREB.
SQ SEQUENCE 217 AA; 23121 MW; 3CE2A0CA25C99CC Q9C64;

Query Match 80.2%; Score 89; DB 11; Length 217;
Best local Similarity 94.7%; Pred. No. 2.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNELSSD 22
   11111111111111111111
DB 73 EILSRPSPSYRKILNELSSD 91
   11111111111111111111

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RA Sasaki H., Sato K., Schenck C., Seya T., Shibata Y., Storch K.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshak Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK015641; BAB29910.1;
DE InterPro: IPR001630; leuzip_CREB.
DI InterPro: IPR003102; PKID.
DI Pfam: PF02173; PKID; 1.
DE PRINTS: PP00041; LEUZIPPCCREB.
SQ SEQUENCE 196 AA; 20488 MW; B41D48FF61496AC Q9C64;

Query Match 80.2%; Score 89; DB 11; Length 196;
Best local Similarity 94.7%; Pred. No. 2.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNELSSD 22
   11111111111111111111
DB 73 EILSRPSPSYRKILNELSSD 91
   11111111111111111111

RESULT 11
Q9D403 PRELIMINARY; PRI: 217 AA.
AC Q9D403;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DI 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DI 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Adult male testis cDNA, RIKEN full-length enriched library,
DE clone:4930557B01, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi T., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gajbort T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli F., Harsh G.,
RA Blake J., Boffelli P., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nardone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenck C., Seya T., Shibata Y., Storch K.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshak Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK016156; BAB30130.1;
DE InterPro: IPR001630; leuzip_CREB.
DI InterPro: IPR002102; PKID.
DI Pfam: PF02173; PKID; 1.
DE PRINTS: PP00041; LEUZIPPCCREB.
SQ SEQUENCE 217 AA; 23121 MW; 3CE2A0CA25C99CC Q9C64;

Query Match 80.2%; Score 89; DB 11; Length 217;
Best local Similarity 94.7%; Pred. No. 2.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNELSSD 22
   11111111111111111111
DB 73 EILSRPSPSYRKILNELSSD 91
   11111111111111111111

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RESULT 12
Q14501
ID Q14501 PRELIMINARY: PRI: 242 AA.
AC Q14501
DT 01 NOV 2000 (1REMBLrel: 15, Created)
DI 01 OCT 2000 (1REMBLrel: 15, Last sequence update)
DL 01 JUN 2001 (1REMBLrel: 17, Last annotation update)
DE CAMP responsive element modulator (fragment).
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN 111
RP SEQUENCE FROM N.A.
RA Voon K., Lalji E., Scherer S.W., Sassone-Corsi P., Dargatzis N.,
RA Kometani R., Rozman J.
RT "Searches for mutations in the human CAMP responsive element
RT modulator (CREM) gene."
RL Submitted (MAY 2000) to the EMBL/GenBank/DDBJ databases.
LR EMBL: AF213897; AAF68266.2;
LR EMBL: AF212158; AAF68266.2; JOINED.
LR EMBL: AF213897; AAF68266.2; JOINED.
LR EMBL: AF213898; AAF68266.2; JOINED.
LR InterPro: IPR001630; Leuzip_CREB.
LR Pfam: PF00170; bZIP; 1.
LR PRINTS: PR00041; LEUZIP_CREB.
LR NON REP: 242 242
SQ SEQUENCE 242 AA: 24429 MW: 2612084887.318 CRC64;

Query Match 80.2% Score 89; DB 4; Length 242;
Best Local Similarity 94.7% Pred. No. 2,66 06;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 EILSRPSPYRKILNDESSD 22
ID 111 EILSRPSPYRKILNDESSD 141
DB 113 EILSRPSPYRKILNDESSD 141

RESULT 13
Q14501
ID Q14501 PRELIMINARY: PRI: 242 AA.
AC Q14501
DI 01 NOV 1996 (1REMBLrel: 01, Created)
DI 01 NOV 1996 (1REMBLrel: 01, Last sequence update)
DL 01 MAR 2002 (1REMBLrel: 20, Last annotation update)
DE HPEM alpha protein.
GN CREM 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN 111
RP SEQUENCE FROM N.A.
RA Fujimoto T., Fujisawa J., Yoshida M.
RT "Novel isoforms of human cyclic AMP responsive element modulator
RT (CREM) mRNA."
RL Biochem. 115:298-303(1994).
DI SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DI SIMILARITY: BELONGS TO THE bZIP FAMILY.
LR EMBL: D14425; BAA0362.1;
LR InterPro: IPR001630; Leuzip_CREB.
LR Pfam: PF00170; bZIP; 1.
LR PRINTS: PR00041; LEUZIP_CREB.
LR SMART: SM00438; bZIP_BASIC; 1.
LR PROSITE: PS00036; bZIP_BASIC; 1.
KW DNA binding, Nuclear protein.
SQ SEQUENCE 278 AA: 46423 MW: 4734960180.643 CRC64;

Query Match 80.2% Score 89; DB 11; Length 278;
Best Local Similarity 94.7% Pred. No. 3,29 06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPYRKILNDESSD 22
ID 110 EILSRPSPYRKILNDESSD 128
DB 110 EILSRPSPYRKILNDESSD 128

RESULT 15
Q16116
ID Q16116 PRELIMINARY: PRI: 352 AA.
AC Q16116
DI 01 NOV 1996 (1REMBLrel: 01, Created)
DI 01 NOV 1996 (1REMBLrel: 01, Last sequence update)
DL 01 MAR 2002 (1REMBLrel: 20, Last annotation update)
DE cyclic AMP-responsive element modulator.
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE:94128610; PubMed 7916662;
RA Masquillier D., Foulkes N.S., Matteo M.G., Sassone-Corsi P.
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KW DNA binding, Nuclear protein.
SQ SEQUENCE 246 AA: 27568 MW: 2686771000.000 CRC64;

Query Match 80.2% Score 89; DB 4; Length 246;
Best Local Similarity 94.7% Pred. No. 2,86 06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPYRKILNDESSD 22
ID 111 EILSRPSPYRKILNDESSD 141
DB 80 EILSRPSPYRKILNDESSD 98

RESULT 14
Q63884
ID Q63884 PRELIMINARY: PRI: 278 AA.
AC Q63884
DI 01 NOV 1996 (1REMBLrel: 01, Created)
DI 01 NOV 1996 (1REMBLrel: 01, Last sequence update)
DL 01 MAR 2002 (1REMBLrel: 20, Last annotation update)
DE CREM-epsilon.
GN CREM OR CREM EPSILON.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10095;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE:93361150; PubMed 8102791;
RA Bradley T., Blake D., Boulton M.
RT "Protein Kinase A dependent activator in transcription factor CREB
RT reveals new role for CREM repressors."
RL Nature 364:321-324(1991).
DI SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DI SIMILARITY: BELONGS TO THE bZIP FAMILY.
LR EMBL: S64590; AAR27893.1;
LR M3D: M31:88495; Crem.
LR InterPro: IPR001630; Leuzip_CREB.
LR InterPro: IPR004102; PK1b.
LR InterPro: IPR004827; TF_bZIP.
LR Pfam: PF00170; bZIP; 1.
LR Pfam: PF02173; PK1b; 1.
LR PRINTS: PR00041; LEUZIP_CREB.
LR SMART: SM00438; bZIP_BASIC; 1.
LR PROSITE: PS00036; bZIP_BASIC; 1.
KW DNA binding, Nuclear protein.
SQ SEQUENCE 278 AA: 46423 MW: 4734960180.643 CRC64;

Query Match 80.2% Score 89; DB 11; Length 278;
Best Local Similarity 94.7% Pred. No. 3,29 06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPYRKILNDESSD 22
ID 110 EILSRPSPYRKILNDESSD 128
DB 110 EILSRPSPYRKILNDESSD 128

RESULT 15
Q16116
ID Q16116 PRELIMINARY: PRI: 352 AA.
AC Q16116
DI 01 NOV 1996 (1REMBLrel: 01, Created)
DI 01 NOV 1996 (1REMBLrel: 01, Last sequence update)
DL 01 MAR 2002 (1REMBLrel: 20, Last annotation update)
DE cyclic AMP-responsive element modulator.
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE:94128610; PubMed 7916662;
RA Masquillier D., Foulkes N.S., Matteo M.G., Sassone-Corsi P.
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RF "Human CREM gene: evolutionary conservation, chromosomal localization,  
RF and inducibility of the transcript.";  
R2 Cell Growth Differ. 4:931-937(1993).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.  
DR EMBL: S68271; AAC60616.2; -.  
DR InterPro: IPR001630; Leuzip\_CREB.  
DR InterPro: IPR002112; Leuzip\_Jun.  
DR InterPro: IPR004102; PKID.  
DR InterPro: IPR004827; TF\_BZIP.  
DR Pfam: PF00170; bZIP; 1.  
DR Pfam: PF02173; PKID; 1.  
DR PRINTS: PR00041; LEUZIPPRCREB.  
DR PRINTS: PR00043; LEUZIPPRJUN.  
DR SMART: SM00338; BRLZ; 1.  
DR PROSITE: PS00036; BZIP\_BASIC; 1.  
KW DNA-binding; Nuclear protein.  
SQ SEQUENCE 232 AA; 25817 MW; PIP091P6CC797A26 CRC64;

Query Match 80.2%; Score 89; DB 4; Length 332;  
Best local Similarity 94.7%; Pred. No. 3.8e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRRPYSYKKILNDLSSD 22  
IIIIIIIIIIIIIIIIIIII  
Db 113 EILSRRPYSYKKILNDLSSD 131

Search completed: January 2, 2003, 12:30:43  
Job time : 26.5 secs

GenCore version 5.1.1.3  
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com protein protein search, using sw model

Run on: January 2, 2003, 12:25:33, Search time 7 seconds  
(without alignment)  
136,279 Million cell updates/sec

Hit list: 98 99 799 417 1  
Perfect score: 111  
Sequence: 1 LSSELSRRRSYPRKLNLSLSDI 23

Scoring table: BLASTSUM62  
Gapop 10.0, Gapext 0.5

Aligned: 112892 seqs, 4147628 residues

Total number of hits satisfying chosen parameters: 112892

Minimum hit seq length: 0  
Maximum hit seq length: 200000000

Post processing: Minimum Match ok  
Maximum Match 100%  
Fastest first 45 summaries

Databases: SwissProt 40.4\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	83.8	425	1 CREB_BOVIN	P27925 bos taurus
2	93	83.8	441	1 CREB_HUMAN	P16220 homo sapien
3	93	83.8	441	1 CREB_MOUSE	G01147 mus muscula
4	93	83.8	441	1 CREB_RAT	P15337 rattus norv
5	89	80.2	229	1 CREM_HUMAN	G03060 homo sapien
6	89	80.2	341	1 CREM_MOUSE	P27699 mus musculu
7	89	80.2	341	1 CREM_RAT	G03061 rattus norv
8	89	80.2	444	1 CREM_CANFA	P79145 canis fami1
9	75	67.6	217	1 CREB_HYDRA	P51985 hydra atten
10	75	67.6	249	1 CREB_CHLVR	P51984 chlorohydra
11	75	67.6	269	1 AIF1_MOUSE	P81269 mus musculu
12	75	67.6	271	1 AIF1_HUMAN	P18846 homo sapien
13	47	42.3	666	1 YAK5_MYCPN	P25079 mycoplasma
14	47	42.3	1198	1 JAK3_RAT	P22772 rattus norv
15	47	42.3	1299	1 JAK3_MOUSE	G62137 mus musculu
16	45	40.5	593	1 STR2_HUMAN	Q15833 homo sapien
17	45	40.5	692	1 SPE1_HYDRA	G19227 glycerine max
18	45	40.5	702	1 SPE1_ARATH	G95164 arabidopsis
19	44	39.3	337	1 VF11_VACCP	P29888 vaccinia vi
20	44	39.3	354	1 VF11_VACCG	P21052 vaccinia vi
21	44	39.3	406	1 SPE2_THEOC	G01160 theobroma c
22	44	39.3	711	1 SPE2_APATB	G21141 arabidopsis
23	44	39.3	908	1 Y066_NPVAC	P41467 autographa
24	44	39.3	1124	1 JAK2_HUMAN	P52333 homo sapien
25	44	39.3	1132	1 JAK2_HUMAN	G06674 homo sapien
26	44	39.3	1180	1 TYK2_MOUSE	G91117 mus musculu
27	44	39.3	1187	1 TYK2_HUMAN	P29597 homo sapien
28	44	39.3	4421	1 FEZ1_HSVBR	P28955 equine herp
29	43.5	39.2	116	1 Y04E_BACSU	P45902 bacillus su
30	43	38.7	427	1 SYH_MYCLE	P46696 mycobacteri
31	43	38.7	510	1 PUR1_MYCLE	P28173 gallus gall
32	43	38.7	576	1 SYP_HELPD	G92m16 helicobacte
33	43	38.7	577	1 SYP_HELPY	P56124 helicobacte

RESULT 1

CREB\_BOVIN

ID	CREB_BOVIN	STANDARD	PKI	325 AA
AC	P27925; 018957;			
DT	01-AUG-1992 (Rel. 23, created)			
DT	16-OCT-2001 (Rel. 43, last sequence update)			
DT	15-JUN-2002 (Rel. 41, last annotation update)			
DE	cAMP response element binding protein 2 (CREB2) (cyclic AMP responsive DNA binding protein).			
GN	CREB2.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID 9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE 92119333; PubMed 1837490;			
RA	Willemis L., Kottmann R., Chen G., Portetelle D., Burny A., Boerse D.,			
RT	"Nucleotide sequence of the bovine cyclic AMP responsive DNA binding			
RT	protein (CREB2) cDNA."			
KL	JNA Seq. 1:419-417(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Adam P., Twizore J.C., Burny A., Kottmann R., Willemis L.,			
RL	Submitted (MAY 1997) to the EMBL/Genbank/DBR databases.			
RN	[3]			
RP	FUNCTION.			
RX	MEDLINE 92114179; PubMed 1409910;			
RA	Willemis L., Kottmann R., Chen G., Portetelle D., Burny A., Boerse D.,			
RT	"A cyclic AMP-responsive DNA-binding protein (CREB2) is a cellular			
RT	transactivator of the bovine leukemia virus long terminal repeat."			
KL	J. Virol. 66:766-772(1992).			
RN	[4]			
RP	FUNCTION.			
RX	MEDLINE 94335101; PubMed 8057465;			
RA	Adam P., Fekke J.S.P., Kottmann R., Burny A.,			
RA	Brocmanus L., Willemis L.,			
RT	"Involvement of the cyclic AMP-responsive element binding protein in			
RT	bovine leukemia virus expression in vivo."			
KL	J. Virol. 68:5845-5853(1994).			
RN	[5]			
RP	FUNCTION.			
RX	MEDLINE 96190603; PubMed 8627726;			
RA	Adam P., Kerkhofs P., Kummerick M., Burny A., Kottmann R., Willemis L.,			
RT	"The CREB, ATF-1, and ATF-2 transcription factors from bovine leukemia			
RT	virus infected B lymphocytes activate viral expression."			
KL	J. Virol. 70:1990-1999(1996).			
CC	1 FUNCTION. THIS PROTEIN BINDS THE CAMP RESPONSIVE ELEMENT (CRE).			
CC	A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREB			
CC	STIMULATES TRANSCRIPTION BINDING TO THE CRE.			
CC	1-1 SUBUNIT BINDS DNA AS A DIMER.			
CC	1 SUBCELLULAR LOCATION: Nuclear.			
CC	1-1 PIM: CREB IS STIMULATED BY PHOSPHORYLATION.			
CC	1-1 SIMILARITY: BELONGS TO THE BZIP FAMILY.			

ALIGNMENTS

44	43	48.7	593	1	STR2_CANFA	Q28288 canis fami1
45	43	48.7	593	1	STR2_MOUSE	Q04324 mus musculu
46	43	48.7	594	1	STR2_RAT	Q02753 rattus norv
47	43	48.7	659	1	STR2_SYNY3	P22587 synchocyst
48	43	48.7	1131	1	CHS1_YEAST	P08004 saccharomyce
49	43	48.7	1493	1	ERC6_HUMAN	Q04468 homo sapien
40	42	37.8	175	1	H3_CANAL	P08898 caenorhabdi
41	42	37.8	206	1	YFF32_41	I33315 escherichia
42	42	37.8	303	1	CHEV_BACSU	P37599 bacillus su
43	42	37.8	336	1	Y04B_MELIDA	Q58743 methanococ
44	42	37.8	441	1	COA1_SCEMV	P16627 soybean chl
45	42	37.8	451	1	NM1_CANAL	P30418 candida alb

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DR EMBL: X57031; CAA40347.1; -;  
DR EMBL: AF006042; AAB62381.1; -;  
DR PIR: S23007; S23007;  
DR InterPro: IPR001639; Leuzip\_CREB;  
DR InterPro: IPR004927; TF\_bZIP;  
DR Pfam: PF00170; bZIP; 1;  
DR Pfam: PF02173; PKID; 1;  
DR PRINTS: PR00041; LEUZIFERCREB;  
DR SMART: SM00438; BRIZ; 1;  
DR PROSITE: PS00036; BZIP\_BASIC; 1;  
KW Transcription regulation; DNA-binding; Activator; Phosphorylation;  
KW Nuclear protein;  
FT DNA\_BIND 268 293 BASIC MOTIF;  
FT DOMAIN 295 316 Transcription factor;  
FT CONFLICT 60 61 QF -- TK (IN RFF 1)  
SQ SEQUENCE 325 AA; 44877 MW; 61B4B4244FAB474B CRC64;

Query Match 83.8%; Score 93; DB 1; Length 325;

Best local Similarity 100.0%; Pred. No. 4e 07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 4 EILSRPSPYRKILNDLSSD 22

DB 110 EILSRPSPYRKILNDLSSD 128

#### RESULT 2

##### CREB\_HUMAN

ID CREB\_HUMAN STANDARD; PRT; 341 AA.  
AC P15220; P21934; Q9DMA7;  
DT 01-APR-1990 (Rel. 14, Created)  
DI 01-MAY 1991 (Rel. 18, Last sequence update)  
DI 15-JUN 2002 (Rel. 41, Last annotation update)  
DE CAMP response element binding protein (CREB).  
GN CREB1.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90219091; PubMed=2142528;  
RA Berkowitz J.A., Gilman M.Z.;  
RT "Two distinct forms of active transcription factor CREB (cAMP  
RT response element binding protein).";  
PL Proc. Natl. Acad. Sci. U.S.A. 97:5259-5262(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90316112; PubMed=2196176;  
RA Yoshimura T., Fujisawa J.I., Yoshida M.;  
RT "Multiple cDNA clones encoding nuclear proteins that bind to the tax-  
RT dependent enhancer of HTLV-1: all contain a leucine zipper structure  
RT and basic amino acid domain.";  
RL EMBO J. 9:2537-2542(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92087371; PubMed=1966745;  
RA Waechter G., Meyer T.E., Hoefler J.P., Habener J.P.;  
RT "Diversification of cyclic AMP-responsive enhancer binding proteins-  
RT generated by alternative exon splicing.";  
RL Trans. Assoc. Am. Physicians 103:28-37(1999).  
RN [4]  
RP SEQUENCE OF 1 87 AND 102-341 FROM N.A.  
RX MEDLINE=89072714; PubMed 2974179;

FA EMBL: J1.P., Meyer T.E., Yip Y., Jameson J.L., Habener J.P.;  
RT "Cyclic AMP-responsive DNA binding protein: structure based on a  
RT cloned placental cDNA.";  
RL Science 242:1430-1433(1988).  
RN [5]  
RP SEQUENCE OF 1 87 AND 102-341 FROM N.A.  
RX MEDLINE 91334144; PubMed 1831258;  
RA Short M.L., Manohar C.P., Furtado M.R., Ghadge G.D., Wolinsky S.M.;  
RT "Nucleotide and derived amino acid sequences of the CRE-binding  
RT proteins from rat C6 glioma and HeLa cells.";  
RL Nucleic Acids Res. 19:4290-4290(1991).  
RN [6]  
RP SEQUENCE OF 1 8 FROM N.A.  
RX MEDLINE=93145890; PubMed=8381074;  
EA Meyer T.E., Waechter G., Yip J., Beckmann W., Habener J.P.;  
RT "The promoter of the gene encoding 37.5% cyclic adenosine  
RT monophosphate (cAMP) response element binding protein contains  
RT cAMP response elements: evidence for positive autoregulation of gene  
RT transcription.";  
RL Endocrinology 132:770-780(1993).  
CC 1 FUNCTION. THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE).  
CC A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREB  
CC STIMULATES TRANSCRIPTION OR BINDING TO THE CRE.  
CC 1 SUBUNIT. BINDS DNA AS A DIMER.  
CC 1 SUBCELLULAR LOCATION: Nuclear.  
CC 1 ALTERNATIVE PRODUCTS: 2 ISOFORMS: CREB-A (SHOWN HERE) AND CREB-  
CC B; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC 1 PTM. STIMULATED BY PHOSPHORYLATION.  
CC 1 SIMILARITY: BELONGS TO THE BZIP FAMILY.

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CC or send an email to [license@sib.sib.ch](mailto:license@sib.sib.ch)).

DR EMBL: S72459; AAB20597.1; -;  
DR EMBL: X55545; CAA39151.1; -;  
DR EMBL: M24356; AAA35717.1; -;  
DR EMBL: M34356; AAA35716.1; -;  
DR EMBL: M27691; AAA35715.1; -;  
DR EMBL: X60003; CAA42620.1; -;  
DR EMBL: S53724; AAD13869.1; -;  
DR PIR: A35769; A35769;  
DR PIR: B35769; B35769;  
DR PIR: B37340; B37340;  
DR PIR: S12561; S12561;  
DR PIR: S22298; S22298;  
DR TRANSFAC; T00163; -;  
DR TRANSFAC; T00166; -;  
DR Genew; HGNC:2345; CREB1.  
DR MIM; 123810; -;  
DR InterPro: IPR001630; Leuzip\_CREB;  
DR InterPro: IPR004827; TF\_bZIP;  
DR InterPro: IPR003102; PKID;  
DR Pfam; PF00170; bZIP; 1;  
DR Pfam; PF02173; PKID; 1;  
DR PRINTS; PR00041; LEUZIFERCREB;  
DR SMART; SM00438; BRIZ; 1;  
DR PROSITE; PS00036; BZIP\_BASIC; 1;  
KW Transcription regulation; DNA-binding; Activator; Phosphorylation;  
KW Nuclear protein; Alternative splicing;  
FT DNA\_BIND 284 305 BASIC MOTIF;  
FT DOMAIN 311 342 LEUCINE-ZIPPER;  
FT VAPSPIC 98 101 MISSING (IN ISOFORM CREB P).  
FT CONFLICT 4 4 E > D (IN REF. 5).  
FT CONFLICT 8 8 E > D (IN REF. 5).  
FT CONFLICT 160 160 T > A (IN REF. 5).  
FT CONFLICT 167 167 T > A (IN REF. 5).  
FT CONFLICT 169 169 T > A (IN REF. 5).

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FI CONFIDENT 176 176 2 3 3 (IN REF. 5)
FI CONFIDENT 184 184 3 3 3 (IN REF. 5)
FI CONFIDENT 188 188 5 5 5 (IN REF. 5)
FI CONFIDENT 195 195 5 5 5 (IN REF. 5)
FI CONFIDENT 210 210 5 5 5 (IN REF. 5)
SQ SEQUENCE 341 AA: 36688 MW: 156983AE40BF69AF CRE664;

Query Match 83.8% Score 93; DB 1; Length 341;
Best Local Similarity 100.0%; Pred. No. 4; 4e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 4 EILSRKPSYRKIIINDLSSD 22
DB 126 EILSRKPSYRKIIINDLSSD 144

RESULT 3
CREB_MOUSE
ID CREB_MOUSE STANDARD; PRI: 341 AA.
AC Q01147;
DT 01 JUN 1994 (Rel. 29, Created)
DI 01 JUN 1994 (Rel. 29, Last sequence update)
DE 15 JUN 2002 (Rel. 41, Last annotation update)
DE CAMP response element binding protein (CREB).
GN CREB1 OR CREB 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI TaxID 10090;
RN [1]
PE SEQUENCE FROM N.A.
RX MEDLINE 92224869; PubMed 1532935;
RA Ruppert S., Cole L.J., Boshart M., Schmid E., Schuetz G.,
RA "Multiple mRNA isoforms of the transcription activator protein CREB:
RA generation by alternative splicing and specific expression in primary
RA spermatocytes."
RL EMBO J. 11:1503-1512(1992).
RN [2]
PE SEQUENCE FROM N.A.
RX MEDLINE 92224867; PubMed 1487109;
RA Cole L.J., Copeland N.G., Gilbert D.J., Jenkins N.A., Schuetz G.,
RA Ruppert R.;
RA "The mouse CREB (cAMP responsive element binding protein) gene:
RA structure, promoter analysis, and chromosomal localization."
RL Genomics 13:974-982(1992).
CC 1 FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE).
CC A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREB
CC STIMULATES TRANSCRIPTION ON BINDING TO THE CRE.
CC 1 SUBUNIT: BINDS DNA AS A DIMER.
CC 1 SUBCELLULAR LOCATION: Nuclear.
CC 1 ALTERNATIVE PRODUCTS: AT LEAST SIX FORMS OF CREB ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC 1 PIM: STIMULATED BY PHOSPHORYLATION.
CC 1 SIMILARITY: BELONGS TO THE BZIP FAMILY.

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EMBL: X67719; CAA47953.1; JOINED.
EMBL: X67721; CAA47953.1; JOINED.
EMBL: X67724; CAA47953.1; JOINED.
EMBL: X67725; CAA47953.1; JOINED.
EMBL: X67726; CAA47953.1; JOINED.
EMBL: X67727; CAA47953.1; JOINED.
EMBL: X67728; CAA47953.1; JOINED.
EMBL: X67719; CAA47953.1; JOINED.
EMBL: X67721; CAA47953.1; JOINED.
EMBL: X67722; CAA47953.1; JOINED.

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DR EMBL: X67724; CAA47953.1; JOINED.
DR EMBL: X67725; CAA47953.1; JOINED.
DR EMBL: X67726; CAA47953.1; JOINED.
DR EMBL: X67727; CAA47953.1; JOINED.
DR EMBL: X67728; CAA47953.1; JOINED.
DR EMBL: M95106; CAA47953.1; JOINED.
DR F1R: S42699; S42699.
DR TRANSFAC: T00989;
DR MGI: MGI:88494; Creb1.
DR InterPro: IPR001630; bzip CREB.
DR InterPro: IPR004827; bZIP.
DR Pfam: PF00170; bZIP; 1.
DR Pfam: PF02173; PKID; 1.
DR PRINTS: PR00041; LEUZIPPREREG.
DR SMART: SM00338; REL2; 1.
DR PROSITE: PS00036; BZIP_BASIC; 1.
KW Transcription regulation; DNA-binding; Activator; Phosphorylation;
KW Nuclear protein; Alternative splicing.
FT DNA_BIND 284 309 BASIC motif (BY SIMILARITY).
FT DOMAIN 311 332 LEUZIP ZIPPER (BY SIMILARITY).
FT VAKSPIC 88 101 MISSING (IN ISOFORM CREB-DELTA).
SQ SEQUENCE 341 AA: 36674 MW: 32958DE917498A CRE64;

Query Match 83.8% Score 93; DB 1; Length 341;
Best Local Similarity 100.0%; Pred. No. 4; 4e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 4 EILSRKPSYRKIIINDLSSD 22
DB 126 EILSRKPSYRKIIINDLSSD 144

RESULT 4
CREB_RAT
ID CREB_RAT STANDARD; PRI: 341 AA.
AC P15337;
DT 01 APR 1990 (Rel. 14, Created)
DI 01 APR 1990 (Rel. 14, Last sequence update)
DI 15 JUN 2002 (Rel. 41, Last annotation update)
DE CAMP-response element binding protein (CREB).
GN CREB1 OR CREB-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI TaxID 10116;
RN [1]
PE SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE 89143746; PubMed 2521922;
RA Gonzalez G.A., Yamamoto K.K., Fischer W.H., Hart D., Menzel P.,
RA Riggs W. III, Vale W.W., Montminy M.R.;
RA "A cluster of phosphorylation sites on the cyclic AMP regulated
RA nuclear factor CREB predicted by its sequence."
RL Nature 337:749-752(1989).
RN [2]
PE SEQUENCE OF 1-87 AND 102-341 FROM N.A. (DELTA ISOFORM).
RX MEDLINE 91334144; PubMed 1831258;
RA Short M.L., Mahesh C.F., Fattado M.R., Ghadon G.D., Watkins S.M.,
RA Thimmapaya B., Jundmann R.A.;
RA "Analysis of rat derived amino acid sequences of the CRE binding
RA proteins from rat C6 glioma and B6a cells."
RL Nucleic Acids Res. 19:4290-4290(1991).
CC 1 FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE).
CC A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREB
CC STIMULATES TRANSCRIPTION ON BINDING TO THE CRE.
CC 1 SUBUNIT: BINDS DNA AS A DIMER.
CC 1 SUBCELLULAR LOCATION: Nuclear.
CC 1 ALTERNATIVE PRODUCTS: TWO FORMS OF CREB CAN BE GENERATED BY
CC ALTERNATIVE SPLICING.
CC 1 PIM: STIMULATED BY PHOSPHORYLATION.
CC 1 SIMILARITY: BELONGS TO THE BZIP FAMILY.

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DR EMBL: X14788; CAA32890.1; -;  
DR EMBL: X60002; CAA42619.1; -;  
DR PIR: S03343; S03343;  
DR PIR: S22299; S22299;  
DR TRANSFAC: T00164; -;  
DR TRANSFAC: T00165; -;  
DR InterPro: IPR001630; Leuzip\_CREP.  
DR InterPro: IPR004827; TF\_BZIP.  
DR InterPro: IPR003102; PKID.  
DR Pfam: PF00170; BZIP; 1.  
DR Pfam: PF02173; PKID; 1.  
DR Pfam: PF02173; PKID; 1.  
DR PRINTS: PR00041; LEUZIP\_CREP.  
DR PRINTS: PR00038; BRL2; 1.  
DR SMART: SM00336; BZIP\_BASIC; 1.  
DR PROSITE: PS00036; BZIP\_BASIC; 1.  
DR PROSITE: PS00036; BZIP\_BASIC; 1.  
DR Transcription factor binding site (TBS) (By similarity).  
KW Nuclear protein; Alternative splicing.  
FT DNA\_BIND 284 309 BASIC MOTIF.  
FT DOMAIN 311 332 LEUCINE-ZIPPER.  
FT VARSPLOT 88 101 MISSING (IN ISOFORM CREB DELTA).  
FT CONFLICT 126 135 E - K (IN REF. 2).  
FT CONFLICT 319 319 E - K (IN REF. 2).  
SQ SEQUENCE 341 AA; 36633 MW; FC08AC5A335D4C2E CRC64;

Query Match 83.8%; Score 93; DB 1; Length 341;  
Best local similarity 100.0%; Pred No. 4; 3e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPPSYRKILNLSDD 22

DB 126 EILSRPPSYRKILNLSDD 144

## RESULT 6

CREM\_HUMAN STANDARD; PRT; 220 AA.  
AC Q03060;  
DI 01-JUN-1994 (Rel. 29, Created)  
DI 01-JUN-1994 (Rel. 29, Last sequence update)  
DI 15-JUN-2002 (Rel. 41, Last annotation update)  
DE CAMP responsive element modulator, alpha isoform  
GN CREM.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE: placenta;  
RX MEDLINE 93096608; PubMed=1461747;  
RA Meyer T.E., Habener J.F.;  
RT "Cyclic AMP response element binding protein CREB and modulator  
RT protein CREM are products of distinct genes".  
RI Nucleic Acids Res. 20:6106-6106(1992).  
CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE).  
CC A SEQUENCE PRESENT IN MANY VITAL AND CELLULAR PROMOTERS, CREM  
CC ALPHA, BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP  
CC TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.  
CC -1- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA (SHOWN HERE), BETA, GAMMA  
CC AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY)  
CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.

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CC or send an email to [license@sib-sb.ch](mailto:license@sib-sb.ch)).

DR EMBL: Z15159; CAA78858.1; -;  
DR PIR: S26685; S26685;  
DR TRANSFAC: T01803; -;  
DR Genew: HGNC:2352; CREM.  
DR MIM: 123912; -;  
DR InterPro: IPR001630; Leuzip\_CREP.  
DR InterPro: IPR004827; TF\_BZIP.  
DR InterPro: IPR003102; PKID.  
DR Pfam: PF00170; BZIP; 1.  
DR Pfam: PF02173; PKID; 1.  
DR PRINTS: PR00041; LEUZIP\_CREP.  
DR SMART: SM00338; BRL2; 1.  
DR PROSITE: PS00036; BZIP\_BASIC; 1.  
DR Transcription regulation, DNA binding, Repressor, Phosphorylation;  
KW Nuclear protein; Alternative splicing.  
FT DNA\_BIND 153 174 BZIP\_BASIC (BY SIMILARITY).  
FT DOMAIN 190 211 LEUCINE ZIPPER (BY SIMILARITY).  
SQ SEQUENCE 220 AA; 24307 MW; 81C504316F825AED CRC64;

Query Match 83.2%; Score 93; DB 1; Length 220;  
Best local similarity 94.7%; Pred No. 1; 1e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPPSYRKILNLSDD 22

DB 64 EILSRPPSYRKILNLSDD 82

## RESULT 6

CREM\_MOUSE STANDARD; PRT; 341 AA.  
AC P27699; P27698;  
DI 01-AUG-1992 (Rel. 23, Created)  
DI 01-AUG-1992 (Rel. 23, Last sequence update)  
DI 15-JUN-2002 (Rel. 41, Last annotation update)  
DE CAMP responsive element modulator.  
GN CREM.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).  
EX MEDLINE 91145994; PubMed=1847666;  
FA Foulkes N.S., Rottrelli E., Sassone-Corsi P.;  
PT "CREM gene: use of alternative DNA-binding domains generates multiple  
PT antagonists of cAMP-induced transcription".  
RI Cell 64:739-749(1991).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM TAU).  
RX MEDLINE 92114938; PubMed=1370576;  
RA Foulkes N.S., Mellstrom B., Benusiglio E., Sassone-Corsi P.;  
RT "Developmental switch of CREM function during spermatogenesis: from  
RT antagonist to activator".  
RI Nature 355:80-84(1992).  
CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE). A  
CC SEQUENCE PRESENT IN MANY VITAL AND CELLULAR PROMOTERS, ISOFORMS  
CC ALPHA, BETA, AND GAMMA ARE ANTAGONISTS OF THE CAMP TRANSCRIPTIONAL  
CC RESPONSE, WHILE ISOFORM TAU IS AN ACTIVATOR.  
CC -1- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA, GAMMA AND TAU  
CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- DEVELOPMENTAL STAGE: IN PREMEIOTIC GERM CELLS, EXPRESSED AT LOW  
CC AMOUNTS IN THE ANTAGONIST FORM. SUBSEQUENTLY, DURING  
CC SPERMATOGENESIS, THE ISOFORM TAU (ACTIVATOR) IS EXPRESSED





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RL Biochem. Biophys. Res. Commun. 237:74-78(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE).
CC A RESPONSE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREM
CC ALPHA, BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP
CC TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.
CC -!- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nucleus.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS, ALPHA, BETA, GAMMA AND DELTA
CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
CC -----
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CC or send an email to license@isb.sib.ch).
CC -----
DR EMBL: X99115; CAA67563.1; -.
DR InterPro: IPR001639; Leuzip_CREB.
DR InterPro: IPR004827; TF_BZIP.
DR InterPro: IPR003102; PKID.
DR Pfam: PF00170; bZIP; 1.
DR PRINTS: PR00041; LEUZIPPCCREB.
DR SMART: SM00338; BRLZ; 1.
DR PROSITE: PS00036; BZIP_BASIC; 1.
KW Transcription regulation, DNA binding, Activator, Repressor;
KW Phosphorylation; Nuclear protein; Alternative splicing.
FT DNA_BIND 287 308 BASIC MOTIF (BY SIMILARITY).
FT DOMAIN 314 335 LEUCINE-ZIPPER (BY SIMILARITY).
SQ SEQUENCE 344 AA; 36915 MW; 7CF50FF3232222919 CRC64;

Query Match 80.2%; Score 89; DB 1; Length 344;
Best Local Similarity 94.7%; Pred. No. 1.8e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKTIINLESD 22
DB 113 EILSRPSPSYRKTIINLESD 131

RESULT 9
CREB_HYDRA1 STANDARD; PRT; 217 AA.
AC P51985;
BI 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE CAMP response element binding protein.
GN CREB.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydrozoa; Hydra.
OX NCBI_TaxID: 6087.
RN [1]
RP SEQUENCE FROM N.A.
PX MEDLINE-95262565; PubMed-7743942;
RA Galliot B., Welsch M., Schaeckel C., Hoffmeister S., Schaller H.C.;
RT "The CAMP response element binding protein is involved in hydra
RL regeneration.";
RL Development 121:1205-1209(1995).
CC -!- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE).
CC SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. COULD
CC REGULATE THE TRANSCRIPTIONAL ACTIVITY OF GENES INVOLVED IN
CC REGENERATION PROCESSES.
CC -!- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
CC -----
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CC -----
DR EMBL: X83873; CAA58753.1; -.
DR InterPro: IPR004827; TF_BZIP.
DR InterPro: IPR003102; PKID.
DR Pfam: PF00170; bZIP; 1.
DR PRINTS: PR02173; PKID; 1.
DR SMART: SM00338; BRLZ; 1.
DR PROSITE: PS00036; BZIP_BASIC; 1.

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CC -----
DR EMBL: X83872; CAA58752.1; -.
DR InterPro: IPR004827; TF_BZIP.
DR InterPro: IPR003102; PKID.
DR Pfam: PF00170; bZIP; 1.
DR PRINTS: PR02173; PKID; 1.
DR PROSITE: PS00036; BZIP_BASIC; 1.
KW Transcription regulation, DNA binding, Nuclear protein;
KW Alternative splicing.
FT DNA_BIND 131 141 BASIC MOTIF (BY SIMILARITY).
FT VARSPLIC 145 162 MISSING (IN ISOFORM BETA).
SQ SEQUENCE 217 AA; 24361 MW; 9AFAEAA179AF598 CRC64;

Query Match 67.6%; Score 75; DB 1; Length 217;
Best Local Similarity 73.7%; Pred. No. 0.00016;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKTIINLESD 22
DB 59 EILSRPSPSYRKTIINLESD 77

RESULT 10
CREB_CHLVR STANDARD; PRT; 249 AA.
AC P51984;
BI 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE CAMP response element binding protein.
GN CREB.
OS Chelodactylus viridissimus (Hydra).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydrozoa; Chlorohydra.
OX NCBI_TaxID: 6082;
RN [1]
RP SEQUENCE FROM N.A.
PX MEDLINE-95262565; PubMed-7743942;
RA Galliot B., Welsch M., Schaeckel C., Hoffmeister S., Schaller H.C.;
RT "The CAMP response element binding protein is involved in hydra
RL regeneration.";
RL Development 121:1205-1209(1995).
CC -!- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE).
CC SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. COULD
CC REGULATE THE TRANSCRIPTIONAL ACTIVITY OF GENES INVOLVED IN
CC REGENERATION PROCESSES.
CC -!- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
CC -----
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CC or send an email to license@isb.sib.ch).
CC -----
DR EMBL: X83873; CAA58753.1; -.
DR InterPro: IPR004827; TF_BZIP.
DR InterPro: IPR003102; PKID.
DR Pfam: PF00170; bZIP; 1.
DR PRINTS: PR02173; PKID; 1.
DR SMART: SM00338; BRLZ; 1.
DR PROSITE: PS00036; BZIP_BASIC; 1.

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KW Transcription factor binding, DNA binding, Nuclear protein.  
PI DNA BIND 192 213 BASIC MOTIF (BY SIMILARITY).  
PI DOMAIN 219 249 LEUCINE ZIPPER (BY SIMILARITY).  
SQ SEQUENCE 249 AA; 27950 MW; 5E998A5D2F75A30B CRC64;

Query Match 67.6%; Score 75; Id 1; Length 249;  
Best Local Similarity 73.7%; Pred. No. 0.00019;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

27 4 EILSRPSYRKILNLSSD 22  
|||||  
60 EILSRPSYRKILNLSSD 78

RESULT 11  
ATF1\_MOUSE STANDARD; PRI: 249 AA.  
AC P81269;

DI 15 JUL 1998 (Rel. 36, Created)  
DI 15 JUL 1998 (Rel. 36, Last sequence update)  
DI 16 OCT 2001 (Rel. 40, Last annotation update)  
DE Cyclic AMP-dependent transcription factor ATF-1 (Activating  
transcription factor 1) (TFR ATF1).  
GN ATF1.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID 10090;

RN 111

RP SEQUENCE FROM N.A.

RX MEDLINE 92176556; PubMed 1541847;

RA Lee M, Ren Chund C, Siu Lion M, Li W, F, Hsieh Y, -p, -

RA Lai M, Z, -

PI "Isolation and characterization of nuclear proteins that bind to T  
cell receptor V beta decamer motif.";

PI Immunol. 149:1906-1912(1992).

CC 1 FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)

(CONSENSUS: 5'-GAGGAGGCA-3'; 3'-A-1206-10014-14 IN MAY

VIRAL AND CELLULAR PROMOTERS. BINDS TO THE TAX-RESPONSIVE ELEMENT  
(TRE) OF HIV-1.

CC 1 SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).

CC 1 SUBCELLULAR LOCATION: Nuclear.

CC 1 SIMILARITY: BELONGS TO THE BZIP FAMILY. ATF SUBFAMILY.

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EMBL: M6372; AAA40395.1;

MDL: M6372; A411.

InterPro: IPR001630; Leuzip CREB.

InterPro: IPR004827; PF\_bZIP.

InterPro: IPR003162; PKID.

Plant: PF00170; bZIP; 1.

Plant: PF02173; PKID; 1.

PRINTS: PF00043; LEUZIPPEREB.

PRINTS: PS00036; BZIP\_BASIC; 1.

KW Transcription regulation; DNA binding; Activator; Nuclear protein.

PI DNA BIND 213 249 BASIC MOTIF.

PI DOMAIN 249 260 LEUCINE ZIPPER.

SQ SEQUENCE 269 AA; 29237 MW; 9885265159164A06 CRC64;

Query Match 67.6%; Score 75; Id 1; Length 269;  
Best Local Similarity 83.9%; Pred. No. 0.00021;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

27 5 EILSRPSYRKILNLSSD 22  
|||||  
1111111111111111

DB 57 EILSRPSYRKILNLSSD 74

RESULT 12

ATF1\_HUMAN

ID ATF1\_HUMAN STANDARD; PRI: 271 AA.

AC P18846; P25168;

DI 01 NOV 1990 (Rel. 16, Created)

DI 01 MAY 1992 (Rel. 22, Last sequence update)

DI 16 OCT 2001 (Rel. 40, Last annotation update)

DE Cyclic-AMP-dependent transcription factor ATF-1 (Activating  
transcription factor 1) (TFRB36 protein).

GN ATF1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea.

OX NCBI\_TaxID 9606;

RN 111

RP SEQUENCE FROM N.A.

RX MEDLINE 90316112; PubMed 2196176;

RA Yoshimura T, Fujisawa J, I, Yoshida M, -

PI "Multiple cDNA clones encoding nuclear proteins that bind to the tax

dependent enhancer of HIV-1; all contain a leucine zipper structure

and basic amino acid domain.";

PI EMBO J. 9:2537-2542(1990).

RN 121

RP SEQUENCE OF 39-271 FROM N.A.

RX MEDLINE 90185187; PubMed 2516827;

RA Hai T, Liu F, Conkos W, J, Green M, K, -

PI "Transcription factor ATF cDNA clones: an extensive family of leucine

zipper proteins able to selectively form DNA binding heterodimers.";

PI Genes Dev. 3:2083-2090(1989).

RN 131

RP ERRATUM.

RA Hai T, Liu F, Conkos W, J, Green M, K, -

PI Genes Dev. 4:682-682(1990).

CC 1 FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)

(CONSENSUS: 5'-GAGGAGGCA-3'; 3'-A-1206-10014-14 IN MANY

VIRAL AND CELLULAR PROMOTERS. BINDS TO THE TAX-RESPONSIVE ELEMENT  
(TRE) OF HIV-1.

CC 1 SUBUNIT: BINDS DNA AS A DIMER.

CC 1 SUBCELLULAR LOCATION: Nuclear.

CC 1 SIMILARITY: BELONGS TO THE BZIP FAMILY. ATF SUBFAMILY.

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EMBL: X55544; CAA39150.1;

PIR: S12560; S12560.

PIR: A34223; A34223.

TRANSFAC: T00968; -

GeneW: HGNC:783; ATF1.

MIM: 123803; -

InterPro: IPR001630; Leuzip CREB.

InterPro: IPR004827; PF\_bZIP.

InterPro: IPR003162; PKID.

Plant: PF00170; bZIP; 1.

Plant: PF02173; PKID; 1.

PRINTS: PS00043; LEUZIPPEREB.

PRINTS: SM00338; BZIP; 1.

PROSITE: PS00036; BZIP\_BASIC; 1.

KW Transcription regulation; DNA binding; Activator; Nuclear protein.

PI DNA\_BIND 215 235 BASIC MOTIF.

PI DOMAIN 241 262 LEUCINE ZIPPER.

PI CONFLIC 55 55 H - A (IN REF. 2).

PI CONFLIC 227 227 MISSING (IN REF. 2).

SQ SEQUENCE 271 AA; 29232 MW; BAFEDF076441373 CRC64;

```
Query Match 67.6%; Score 75; DB 1; Length 271;
Best Local Similarity 93.3%; Pred. No. 0.00021;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0.

QY 5 ILSRPSPSYRFTINLSSP 22
DB 57 ILARPSYRKILNLSSE 74

RESULT 13
YA35_MYCPN STANDARD; PRT; 666 AA.
AC P75079;
DI 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MPN035 (B01_orf666).
GN MPN035 OR MP119.
OS Mycoplasma pneumoniae.
OC Bacteria, Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE-97105985; PubMed-8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Ill R.-G.,
RA Herrmann R.;
RI "Complete sequence analysis of the genome of the bacterium Mycoplasma
RI pneumoniae";
RI Nucleic Acids Res 24:4420-4436(1996).
CC -1- SIMILARITY: BELONGS TO THE MG042 / MG096 / MG288 FAMILY
CC -----
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CC -----
EMBL: AE000014; AAR95767.1;
DI InterPro: IPR001307; MG042/MG096/MG288_1
DE Summary: IPR001307; MG042/MG096/MG288_1
DR Pfam: PF03072; WP0247; 1.
DR Pfam: PF03086; DUF240; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 666 AA; 76898 MW; DF096AA4B475402D CRC64;

Query Match 42.3%; Score 47; DB 1; Length 666;
Best Local Similarity 47.1%; Pred. No. 13;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0.

QY 3 SEILSRPSPSYRKILNVL 19
DB 443 SEILSRPSPSWINLSDI 449

RESULT 14
JAK4_RAI
DI JAK4_RAI STANDARD; PRT; 1100 AA.
AC Q64272;
DI 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase JAK3 (EC 2.7.1.112) (Janus kinase 3) (JAK-3).
GN JAK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Spleen;
```

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RX MEDLINE 94192819; PubMed-8143863;
RA Takahashi T., Shirasawa T.;
RT "Molecular cloning of rat JAK2, a novel member of the JAK family of
RT protein tyrosine kinases.";
RL PERS Lett. 342:124-128(1994).
CC -1- FUNCTION: TYROSINE KINASE OF THE NON RECEPTOR TYPE, INVOLVED IN
CC THE INTERLEUKIN 2 AND INTERLEUKIN 4 SIGNALING PATHWAY.
CC PHOSPHORYLATES STAT6, IRS1, IRS2 AND PI3K.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine + ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
CC ASSOCIATED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: TRANSCRIBED IN A VARIETY OF TISSUES INCLUDING
CC SPLEEN, LUNG, KIDNEY AND INTESTINE.
CC -1- DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS, THE SECOND ONE
CC PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY); WHILE THE
CC PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT POLE FOR
CC DOMAIN 1.
CC -1- PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4 (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -----
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CC -----
EMBL: S28508; BAA05868.1;
HSSP: P11362; IFGK.
DI InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000719; Sub_kinase.
DR InterPro: IPR000980; SH2.
DE Summary: IPR001245; Tyrosine kinase.
DR Pfam: PF00069; pkinase; 2.
DR ProDom: PD000001; Euk_pkinase; 2.
DR ProDom: PD000093; SH2; 1.
DE Summary: SM00295; R41; 1.
DR SMART: SM00295; SH2; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_AIP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 2.
DR PROSITE: PS50001; SH2; FALSE_NEG.
KW Transferrase, Tyrosine protein kinase; AIP-binding; Phosphorylation;
KW SH2 domain; Repeat.
DI DOMAIN 372 472 SH2 (ATYPICAL).
DI DOMAIN 517 777 PROTEIN KINASE 1.
DI DOMAIN 818 1091 PROTEIN KINASE 2.
DI NP_BIND 824 842 AIP (BY SIMILARITY).
DI BINDING 851 851 AIP (BY SIMILARITY).
DI ACT_SITE 945 945 BY SIMILARITY.
DI MOD_RES 976 976 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 1100 AA; 122560 MW; 1D59CA05F4D07EE2 CRC64;

Query Match 42.3%; Score 47; DB 1; Length 1100;
Best Local Similarity 69.2%; Pred. No. 22;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0.

QY 9 REPSPYRKILNLS 20
DB 762 REPSPYRKILNLS 774

RESULT 15
JAK3_MOUSE STANDARD; PRT; 1299 AA.
DI JAK3_MOUSE
AC Q62147; Q61747; Q61746;
DI 01-NOV-1997 (Rel. 35, Created)
```





Genfore version 5.1.3  
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CM protein protein search, using sw model

Run on: January 2, 2003, 12:26:31 : Search time: 32 seconds  
(without alignments)  
69,097 Million cell updates/sec

Title: US 09 786 317-1

Perfect score: 111

Sequence: 1 ISSRLSRPSYRKILNDLSSD 23

Scoring table: BL-SUM62

Gapop 10.0 : Gapext 0.5

Searched: 283224 gaps, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Prod. No. is the number of results predicted by chance, to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	83.8	317	2	S42702 hypothetical prote
2	93	83.8	325	2	S23007 cAMP response elem
3	93	83.8	326	2	A43120 cAMP-responsive en
4	93	83.8	327	2	A35769 cAMP responsive elem
5	93	83.8	327	2	S20955 regulatory protein
6	93	83.8	327	2	S22298 cAMP response elem
7	93	83.8	341	2	S42699 hypothetical prote
8	93	83.8	341	2	B35769 cAMP response elem
9	93	83.8	341	2	S03343 cAMP response elem
10	90	81.1	327	2	S22299 cAMP response elem
11	89	80.2	317	2	S37944 cAMP response elem
12	89	80.2	220	2	S26685 cAMP response elem
13	89	80.2	229	2	B37944 cAMP response elem
14	89	80.2	229	2	A37944 cAMP response elem
15	89	80.2	278	2	S36101 cAMP response elem
16	89	80.2	341	2	S20827 cAMP response elem
17	89	80.2	341	2	S26686 cAMP response elem
18	89	80.2	344	2	S35601 cAMP response elem
19	89	80.2	344	2	S35602 cAMP response elem
20	88	79.3	328	2	A35643 cAMP response elem
21	75	57.6	259	2	A46490 TGF-beta CRE mot
22	75	67.6	271	2	S12560 transcription fact
23	68	52.3	331	2	S26957 hypothetical prote
24	68	52.3	333	2	L26808 hypothetical prote
25	47	42.3	367	2	G90508 GMP synthase, pp-A
26	47	42.3	366	1	S73445 M10-2 homolog Bcl-2
27	47	42.3	1999	2	S19954 protein tyrosine k
28	47	42.3	1100	2	S43377 protein-tyrosine k
29	47	42.3	1299	2	L58401

30	47	42.3	2231	2	L21870 hypothetical prote
31	47	42.3	3113	2	A30116 probable virulence
32	46	41.4	891	2	G41662 100K surface exten
33	45	40.5	692	2	T06594 arginine decarboxy
34	45	40.5	702	2	S21249 arginine decarboxy
35	45	40.5	702	2	A84541 arginine decarboxy
36	45	40.5	865	2	L40170 hypothetical prote
37	45	40.5	1443	2	L31896 hypothetical prote
38	45	40.5	1588	2	L38660 probable transcrip
39	44	39.6	354	2	G42507 F-11, protein vac
40	44	39.6	711	2	L05291 arginine decarboxy
41	44	39.6	805	2	L41810 Ac-MNV of f66, hem
42	44	39.6	808	2	S72858 Ac-MNV 66 protein
43	44	39.6	837	2	L19271 hypothetical prote
44	44	39.6	1124	2	A55747 L-JAK protein tyro
45	44	39.6	1132	2	JW0091 Janus kinase (K2

## ALIGNMENTS

### RESULT 1

S42702

hypothetical protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 08 Dec-2000

C:Accession: S42702

R:Ruppert, S.J. (1995, P.J.7) Boshart, M.J. Schmid, E.J. Schuetz, G.

EMBL J. 11, 1503-1512, 1992

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati

A:Reference number: S20955; MUID:92244889; PMID:1582936

A:Accession: S42702

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-317-80DP

A:Cross references: EMBL:X67726

C:Genetics:

A:Location: 1879-3233, 3133-3137, 3137-3141

C:Superfamily: fos/jun DNA-binding domain homology

Query Match 83.8% Score 93; DB 2; Length 317;

Best Local Similarity 100.0%; Pred. No. 7,46 07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSYRKILNDLSSD 22

|||||

DB 112 EILSRPSYRKILNDLSSD 130

### RESULT 2

S23007

cAMP response element-binding protein CREB.2 bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 08 Jan 1994 #sequence\_revision 10 Nov 1995 #text\_change 05 Nov 1999

C:Accession: S23007

R:Williams, L.J. Kottmann, R.J. Chen, G.J. Portetelle, D.J. Burny, A. Jerse, D.

DNA Seq. 1, 415-417, 1991

A:Title: Nucleotide sequence of the bovine c-jun, c-fos, and c-myc responsive DNA binding protein

A:Reference number: S23007; MUID:9219333; PMID:1873490

A:Accession: S23007

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-325-3W117

A:Cross references: EMBL:X57311, N1834285, F1187:CA640347.1; F1187:Q286

C:Superfamily: fos/jun DNA binding domain homology

C:Keywords: DNA binding; transcription regulation

F.253 Fos/Jomatin, fos/jun DNA-binding domain homology - F.10-

Query Match 83.8% Score 93; DB 2; Length 325;

Best Local Similarity 100.0%; Pred. No. 7,46 07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSYRKILNDLSSD 22



Db 110 EILSRPSPSYRKILINDLSSD 128

## RESULT 3

A40120  
cAMP-responsive enhancer-binding protein CREB human  
C:Species: Homo sapiens (man)  
C:Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 10-Oct-1997  
C:Accession: A40120  
R:Hoeflter, J.P.; Meyer, T.R.; Yun, Y.; Jameson, J.L.; Habener, J.F.  
Science 242, 1430-1433, 1988  
A:Title: Cyclic AMP-responsive DNA binding protein: structure based on a cloned placental  
A:Reference number: A40120, NCID:89072714, PMID:2974175  
A:Accession: A40120  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-326 <RUP>  
A:Cross-references: GR:M27691  
C:Superfamily: fos/jun DNA-binding domain homology  
F:260-303/Domain: fos/jun DNA-binding domain homology <RUP>

Query Match 83.8% Score 93; DB 2; Length 326;  
Best Local Similarity 100.0%; Pred. No. 7.6e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILINDLSSD 22

Db 111 EILSRPSPSYRKILINDLSSD 129

## RESULT 4

A35769  
cAMP response element binding protein A human  
C:Species: Homo sapiens (man)  
C:Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 21-Jul-2000  
C:Accession: A37340; A35769  
R:Maeder, G.; Meyer, T.E.; Hoeflter, J.P.; Habener, J.F.  
Trans. Assoc. Am. Physicians 103, 28-37, 1990  
A:Title: Identification of cyclic AMP responsive enhancer binding proteins generated by  
A:Reference number: A37340, MIMD:92087371, PMID:1966745  
A:Accession: A37340  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-327 <WAE>  
A:Cross-references: GR:M4356; NID:4240429; PIDN:AAA35716 1; PID:q181043  
P:Perkowitz, L.A.; Gilman, M.Z.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5258-5262, 1990  
A:Title: Two distinct forms of active transcription factor CREB (cAMP response element  
A:Reference number: A35769, MIMD:90319291; PMID:2142528  
A:Accession: A35769  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-327 <BER>  
A:Cross-references: GR:M4356; NID:q181042; PIDN:AAA35716 1; PID:q181043  
C:Superfamily: fos/jun DNA-binding domain homology  
C:Keywords: alternative splicing; DNA binding; transcription regulation  
F:261-304/Domain: fos/jun DNA-binding domain homology <RUP>

Query Match 83.9% Score 93; DB 2; Length 327;  
Best Local Similarity 100.0%; Pred. No. 7.6e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILINDLSSD 22

Db 112 EILSRPSPSYRKILINDLSSD 130

## RESULT 5

S20955  
regulatory protein CREB - mouse  
N:Alternate names: cAMP responsive element binding protein  
C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 10-Oct-1997  
C:Accession: S20955

R:Kuppert, S.; Cole, T.J.; Roshart, M.; Schmid, E.; Schuetz, G.  
EMBO J. 11, 1503-1512, 1992

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati  
A:Reference number: S20955; MIMD:92224889; PMID:1522935

A:Accession: S20955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-327 <RUP>

A:Cross-references: EMBL:X67727

C:Genetics:

A:Reference number: S20955; MIMD:92224889; PMID:1522935

C:Superfamily: fos/jun DNA-binding domain homology

F:261-304/Domain: fos/jun DNA-binding domain homology <RUP>

Query Match 92.9% Score 92; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 7.6e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILINDLSSD 22

Db 112 EILSRPSPSYRKILINDLSSD 130

## RESULT 6

S22298  
cAMP response element-binding protein CREB-delta - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
C:Accession: S22298  
R:Short, M.L.; Manohar, C.F.; Portado, M.P.; Chadge, G.D.; Welinsky, S.M.; Thimmappaya  
Nucleic Acids Res. 19, 4290, 1991  
A:Title: Nucleotide and derived amino acid sequences of the CRE binding proteins from  
A:Reference number: S22298; MIMD:91334144; PMID:1831258  
A:Accession: S22298  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-327 <SHO>  
A:Cross-references: EMBL:X60293; NID:43423; PIDN:AAA39900 1; PID:q30494  
A:Note: the nucleotide sequence was submitted to the EMBL data library, May 1991  
C:Superfamily: fos/jun DNA-binding domain homology  
C:Keywords: DNA binding; transcription regulation  
F:261-304/Domain: fos/jun DNA-binding domain homology <RUP>

Query Match 92.9% Score 93; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 7.6e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILINDLSSD 22

Db 112 EILSRPSPSYRKILINDLSSD 130

## RESULT 7

S42699  
hypothetical protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 01-Dec-2000  
C:Accession: S42699; S42700; S42701  
R:Kuppert, S.; Cole, T.J.; Roshart, M.; Schmid, E.; Schuetz, G.  
EMBO J. 11, 1503-1512, 1992  
A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati  
A:Reference number: S20955; MIMD:92224889; PMID:1522935  
A:Accession: S42699  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-341 <RUP>  
A:Cross-references: EMBL:X67727  
A:Accession: S42700  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-101; <SLF> <R02>



A:Cross references: EMBL:X67722

A:Accession: 842701

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 188 (137 - 803)

A:Cross references: EMBL:X67721

C:Notes:

A:Features: 367 (137 - 803) (2003-03-03)

C:Superfamily: Fos/Jun DNA binding domain homology

F:2/5 318/Genbank: fos/jun DNA binding domain homology (EMBL)

Query Match 83.8% Score 93; DB 2; Length 341;

Best Local Similarity 100.0%; Prod. No. 80-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRKPSYRKILNLSDD 22

DB 126 EILSRKPSYRKILNLSDD 144

RESULT 8

845/769

CAMP response element binding protein 1, form B human

N:Alternate names: CREB1, form B

C:Notes: CAMP response element binding protein 1, form A

C:Species: Homo sapiens (human)

C:Date: 05-Oct-1990 #sequence\_revision:05-Oct-1990 #text\_change:21-Jul-2000

C:Accession: B33740; B33769; S12561; 153266

R:Wardner, G.; Meyer, L.E.; Bortler, J.P.; Babener, J.F.

Trans. Assoc. Am. Physicians 103: 28-37, 1990

A:Title: Identification of cyclic AMP-responsive enhancer binding proteins generated by

A:Reference number: A37340; M010:92087371; PMID:11966745

A:Accession: B37340

A:Molecule type: DNA

A:Residues: 1-341 -WAE-

A:Cross references: B3372459

R:Berkowitz, L.A.; Gilman, M.Z.

Proc. Natl. Acad. Sci. U.S.A. 87: 5258-5262, 1990

A:Title: Two distinct forms of active transcription factor CREB (cAMP response element b

A:Reference number: A3769; M010:90319091; PMID:2142528

A:Accession: B33769

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-341 -BER-

A:Cross references: B337356; NID:q181042; PID:AAA35717-1; PID:q181044

R:Yoshimura, I.; Fujisawa, J.I.; Yoshida, M.

EMBL J. 9: 2537-2542, 1990

A:Title: Multiple cDNA clones encoding nuclear proteins that bind to the tax-dependent e

A:Reference number: S12559; M010:90316112; PMID:2196176

A:Accession: S12559

A:Molecule type: mRNA

A:Residues: 1-341 -YGS-

A:Cross references: EMBL:X65645; NID:q187637; PID:AAA39151-1; PID:q287638

R:Meyer, L.E.; Waeber, G.; Lin, J.; Beckmann, W.; Babener, J.F.

Endocrinology 132: 776-780, 1993

A:Title: The promoter of the gene encoding 3',5'-cyclic adenosine monophosphate (cAMP) r

transcription.

A:Reference number: 153266; M010:91145890; PMID:8481074

A:Accession: 153266

A>Status: translated from GB/EMBL/00BJ

A:Molecule type: DNA

A:Residues: 1-9 -PES-

A:Cross references: B3353724; NID:1254454; PID:AAA14869-1; PID:q4261559

C:Notes:

A:Name: GB/CREB1

A:Cross references: GB:119803; OMIM:123810

A:Map position: 2432,3-2434

C:Superfamily: Fos/Jun DNA binding domain homology

C:Keywords: alternative splicing; DNA binding; leucine zipper; transcription factor

F:2/5 318/Genbank: fos/jun DNA binding domain homology (EMBL)

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRKPSYRKILNLSDD 22

DB 126 EILSRKPSYRKILNLSDD 144

RESULT 9

803343

CAMP response element binding protein rat

N:Alternate names: nuclear factor, 48K

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Feb-1990 #sequence\_revision:28-Feb-1990 #text\_change:05-Nov-1999

C:Accession: S03343

R:Gonzalez, G.A.; Yamamoto, K.K.; Fischer, W.H.; Karin, D.; Menzel, P.; Riggs J.L.; W.

Nature 337: 749-752, 1989

A:Title: A cluster of phosphorylation sites on the cyclic AMP-regulated nuclear facto

A:Reference number: S03343; M010:89143746; PMID:2521922

A:Accession: S03343

A:Molecule type: mRNA

A:Residues: 1-341 -GON-

A:Cross references: EMBL:X14788; NID:q56004; PID:AAA2890-1; PID:q56005

A:Note: part of this sequence was confirmed by protein sequencing

C:Superfamily: Fos/Jun DNA binding domain homology

C:Keywords: DNA binding; transcription regulation

F:2/5 318/Genbank: fos/jun DNA binding domain homology (EMBL)

Query Match

Best Local Similarity 100.0%; Prod. No. 80-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRKPSYRKILNLSDD 22

DB 126 EILSRKPSYRKILNLSDD 144

RESULT 10

822299

CAMP response element binding protein CREBdelta rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 19-Feb-1994 #sequence\_revision:10-Nov-1999 #text\_change:05-Nov-1999

C:Accession: S22299

R:Short, M.L.; Manohar, C.F.; Furtado, M.R.; Ghadde, G.D.; Wolinsky, S.M.; Thimmappa

Nucleic Acids Res. 19: 4290, 1991

A:Title: Nucleotide and derived amino acid sequences of the CRE binding proteins from

A:Reference number: S22298; M010:91340144; PMID:1831258

A:Accession: S22299

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-327 -SHO-

A:Cross references: EMBL:X69002; NID:q56008; PID:AAA42619-1; PID:q56009

A:Note: this sequence was submitted to the EMBL Data Library, May 1991

C:Superfamily: Fos/Jun DNA binding domain homology

C:Keywords: DNA binding; transcription regulation

F:2/5 318/Genbank: fos/jun DNA binding domain homology (EMBL)

Query Match

Best Local Similarity 94.7%; Prod. No. 2130-007;

Matches 18; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 4 EILSRKPSYRKILNLSDD 22

DB 112 EILSRKPSYRKILNLSDD 140

RESULT 11

837944

CAMP response element binding protein gamma mouse

C:Species: Mus musculus (house mouse)

C:Date: 12-Jul-1994 #sequence\_revision:12-Jul-1994 #text\_change:05-Nov-1999

C:Accession: C37944

R:Foulkes, N.S.; Borrelli, E.; Sassone-Corsi, P.

Cell 64: 739-749, 1991

A:Title: CREM gene: use of alternative DNA-binding domains generates multiple antagonists

A:Reference number: A37944; MIM:6114594; PMID:1847666

A:Accession: A37944

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-217 <FOU>

A:Cross-references: GB:M60285; NID:q192716; PID:AAA17495.1; PID:q192717

C:Superfamily: fos/jun DNA-binding domain homology

F:151-194/Domain: fos/jun DNA binding domain homology <FJD>

Query Match 80.2% Score 89; DB 2; Length 229;  
Best Local Similarity 94.7% Pred. No. 2.2e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNELSSD 22

|||||

Db 61 EILSRPSPSYRKILNELSSD 79

RESULT 12

S26685

CAMP response element modulator CREM - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21 Jul-2000

C:Accession: S26685

R:Meyer, T.E.; Habener, J.F.

Nucleic Acids Res. 20, 6105, 1992

A:Title: Cyclic AMP response element binding protein CREB and modulator protein CREM are

A:Reference number: S26685; MIM:93096608; PMID:1461747

A:Accession: S26685

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-220 <MEY>

A:Cross-references: EMBL:Z15155; NID:q30216; PID:CAA78858.1; PID:q30217

A:Note: this sequence was submitted to the FIM Data Library, September 1992

C:Genetics:

A:Gene: GDB:CREM

A:Cross-references: GDB:269801

A:Map position: 10p12.1-10p11.2

C:Superfamily: fos/jun DNA-binding domain homology

C:Keywords: DNA binding; heterodimer; leucine zipper; transcription factor

F:154-197/Domain: fos/jun DNA binding domain homology <FJD>

Query Match 80.2% Score 89; DB 2; Length 229;  
Best Local Similarity 94.7% Pred. No. 2.1e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNELSSD 22

|||||

Db 64 EILSRPSPSYRKILNELSSD 82

RESULT 13

B37944

CAMP response element-binding protein beta mouse

C:Species: Mus musculus (house mouse)

C:Date: 12-Jul-1991 #sequence\_revision 12-Jul-1991 #text\_change 05-Nov-1999

C:Accession: B37944

R:Foulkes, N.S.; Borrelli, E.; Sassone-Corsi, P.

Cell 64, 739-749, 1991

A:Title: CREM gene: use of alternative DNA binding domains generates multiple antagonists

A:Reference number: A37944; MIM:91145994; PMID:1847666

A:Accession: B37944

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-229 <FOU>

A:Cross-references: GB:M60285; NID:q192716; PID:AAA17495.1; PID:q192718

C:Superfamily: fos/jun DNA-binding domain homology

F:163-206/Domain: fos/jun DNA-binding domain homology <FJD>

Query Match 80.2% Score 89; DB 2; Length 229;  
Best Local Similarity 94.7% Pred. No. 2.2e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNELSSD 22

|||||

Db 61 EILSRPSPSYRKILNELSSD 79

RESULT 14

A37944

CAMP response element-binding protein alpha - mouse

C:Species: Mus musculus (house mouse)

C:Date: 12-Jul-1991 #sequence\_revision 12-Jul-1991 #text\_change 05-Nov-1999

C:Accession: A37944

R:Foulkes, N.S.; Borrelli, E.; Sassone-Corsi, P.

Cell 64, 739-749, 1991

A:Title: CREM gene: use of alternative DNA-binding domains generates multiple antagon

A:Reference number: A37944; MIM:91145994; PMID:1847666

A:Accession: A37944

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-229 <FOU>

A:Cross-references: GB:M60285; NID:q192716; PID:AAA17497.1; PID:q192719

C:Superfamily: fos/jun DNA-binding domain homology

C:Keywords: alternative splicing; DNA binding; transcription regulation

F:153-206/Domain: fos/jun DNA-binding domain homology <FJD>

Query Match 80.2% Score 89; DB 2; Length 229;

Best Local Similarity 94.7% Pred. No. 2.2e-06;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNELSSD 22

|||||

Db 61 EILSRPSPSYRKILNELSSD 79

RESULT 15

S36101

CAMP response element-binding protein epsilon - mouse

N:Alternate names: cAMP-responsive element modulator epsilon

C:Species: Mus musculus (house mouse)

C:Date: 10-Feb-1993 #sequence\_revision 10-Feb-1993 #text\_change 05-Nov-1999

C:Accession: S36101

R:Prizella, L.; Linker, S.; Montminy, M.

Nature 364, 821-824, 1993

A:Title: Protein kinase A-dependent activation in transcription factor CREB reveals ne

A:Reference number: S36101; MIM:93361150; PMID:8102791

A:Accession: S36101

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-279 <BR>

A:Cross-references: GB:S64590; NID:q108290; PID:AAB27993.1; PID:q108297

C:Superfamily: fos/jun DNA-binding domain homology

F:212-255/Domain: fos/jun DNA binding domain homology <FJD>

Query Match 80.2% Score 89; DB 2; Length 278;

Best Local Similarity 94.7% Pred. No. 2.7e-06;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNELSSD 22

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Db 110 EILSRPSPSYRKILNELSSD 128

Search completed: January 27 2003, 12:29:15

Job time : 33 secs



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; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 326
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CAMP dependent protein kinase interaction fusion protein
US-10-211-088-326

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Query Match      83.8%; Score 93; DB 6; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 EILSRPPSYRKILNLSDD 22
Db      79 EILSRPPSYRKILNLSDD 97

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PRINT
US-09-724-676-67411
; Sequence 67411 Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09-724-676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67411
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-67411

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Query Match      80.2%; Score 89; DB 5; Length 137;
Best Local Similarity 94.7%; Pred. No. 1.9e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      4 EILSRPPSYRKILNLSDD 22
Db      62 EILSRPPSYRKILNLSDD 80

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RESULT 4
US-09-724-676A-67411
; Sequence 67411 Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09-724-676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67411
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-67411

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```

Query Match      80.2%; Score 89; DB 5; Length 137;
Best Local Similarity 94.7%; Pred. No. 1.9e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      4 EILSRPPSYRKILNLSDD 22
Db      62 EILSRPPSYRKILNLSDD 80

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RESULT 5
US-09-724-676-67425

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```

; Sequence 67425 Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09-724-676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67425
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-67425

```

```

Query Match      80.2%; Score 89; DB 5; Length 175;
Best Local Similarity 94.7%; Pred. No. 2.4e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      4 EILSRPPSYRKILNLSDD 22
Db      115 EILSRPPSYRKILNLSDD 133

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RESULT 6
US-09-724-676-67426
; Sequence 67426 Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09-724-676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67426
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-67426

```

```

Query Match      80.2%; Score 89; DB 5; Length 175;
Best Local Similarity 94.7%; Pred. No. 2.4e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      4 EILSRPPSYRKILNLSDD 22
Db      115 EILSRPPSYRKILNLSDD 133

```

```

RESULT 7
US-09-724-676A-67425
; Sequence 67425 Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09-724-676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67425
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-67425

```

```

Query Match      80.2%; Score 89; DB 5; Length 175;
Best Local Similarity 94.7%; Pred. No. 2.4e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      4 EILSRPPSYRKILNLSDD 22

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```

10 115 EILSRPSPYRKILNELSSD 133
;
;
; Sequence 67426, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724676A
; CURRENT FILING DATE: 2000 11 28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 67426
; LENGTH: 175
; TYPE: PRI
; ORGANISM: Homo sapiens
US 09 724 676A 67426

Query Match      80.2%   Score 89;   DB 5;   Length 175;
Best Local Similarity 94.7%   Prod. No. 2,66,06;
Matches 18;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY 4 EILSRPSPYRKILNELSSD 22
DB 115 EILSRPSPYRKILNELSSD 133

RESULT 9
US 09 724 676 67419
; Sequence 67419, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724676A
; CURRENT FILING DATE: 2000 11 28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 67419
; LENGTH: 186
; TYPE: PRI
; ORGANISM: Homo sapiens
US 09 724 676 67419

Query Match      80.2%   Score 89;   DB 5;   Length 186;
Best Local Similarity 94.7%   Prod. No. 2,66,06;
Matches 18;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY 4 EILSRPSPYRKILNELSSD 22
DB 115 EILSRPSPYRKILNELSSD 133

RESULT 10
US 09 724 676A 67419
; Sequence 67419, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724676A
; CURRENT FILING DATE: 2000 11 28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 67419
; LENGTH: 186
; TYPE: PRI
; ORGANISM: Homo sapiens
US 09 724 676A 67419

Query Match      80.2%   Score 89;   DB 5;   Length 186;

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Best Local Similarity 94.7%   Prod. No. 2,66,06;
Matches 18;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY 4 EILSRPSPYRKILNELSSD 22
DB 115 EILSRPSPYRKILNELSSD 129

RESULT 11
US 09 724 676-67427
; Sequence 67427, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724676A
; CURRENT FILING DATE: 2000 11 28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 67427
; LENGTH: 190
; TYPE: PRI
; ORGANISM: Homo sapiens
US 09 724 676-67427

Query Match      80.2%   Score 89;   DB 5;   Length 190;
Best Local Similarity 94.7%   Prod. No. 2,66,06;
Matches 18;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY 4 EILSRPSPYRKILNELSSD 22
DB 115 EILSRPSPYRKILNELSSD 133

RESULT 12
US 09 724-676A-67427
; Sequence 67427, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724676A
; CURRENT FILING DATE: 2000 11 28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 67427
; LENGTH: 190
; TYPE: PRI
; ORGANISM: Homo sapiens
US 09 724-676A-67427

Query Match      80.2%   Score 89;   DB 5;   Length 190;
Best Local Similarity 94.7%   Prod. No. 2,66,06;
Matches 18;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY 4 EILSRPSPYRKILNELSSD 22
DB 115 EILSRPSPYRKILNELSSD 133

RESULT 13
US 09 724 676-67432
; Sequence 67432, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724676A
; CURRENT FILING DATE: 2000 11 28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 67432
; LENGTH: 224

```

TYPE: PRI  
ORGANISM: Homo sapiens  
US-09-724-676-67432

Query Match 80.2%; Score 89; DB 5; Length 224;  
Best local Similarity 94.7%; Pred. No. 3.2e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPPSYRKIIINLSSD 22  
IIIIIIIIIIIIIIIIIIII  
Db 164 EILSRPPSYRKIIINLSSD 182

## RESULT 14

US-09-724-676-67433

Sequence 67433; Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09724,676  
CURRENT FILING DATE: 2000 11 28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 67433  
LENGTH: 224  
TYPE: PRI  
ORGANISM: Homo sapiens  
US-09-724-676-67433

Query Match 80.2%; Score 89; DB 5; Length 224;  
Best local Similarity 94.7%; Pred. No. 3.2e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPPSYRKIIINLSSD 22  
IIIIIIIIIIIIIIIIIIII  
Db 164 EILSRPPSYRKIIINLSSD 182

## RESULT 15

US-09-724-676A-67432

Sequence 67432; Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 67432  
LENGTH: 224  
TYPE: PRI  
ORGANISM: Homo sapiens  
US-09-724-676A-67432

Query Match 80.2%; Score 89; DB 5; Length 224;  
Best local Similarity 94.7%; Pred. No. 3.2e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPPSYRKIIINLSSD 22  
IIIIIIIIIIIIIIIIIIII  
Db 164 EILSRPPSYRKIIINLSSD 182

Search completed: January 2, 2003, 12:35:49  
Job time : 11.5 secs









Query Match	83.4%	Score 93	143.1	Length 328
Best local Similarity	100.0%	Prod. No. 3,460,067		
Matches 19; Conserved 10		Mismatch 3	0	Indels 3

Q7	4	E	I	S	R	P	S	Y	R	K	I	N	I	S	S	22
		I	I	I	I	I	I	I	I	I	I	I	I	I		
Q6	112	E	I	S	R	P	S	Y	R	K	I	N	I	S	S	140

```

RESULTS 7
US 09 420 060 8
: Sequence 8, Application US/09420060
: GENERAL INFORMATION:
: APPLICANT: FOSCH, JANE E.
: APPLICANT: KLOMM, DWIGHT J.
: TITLE OF INVENTION: METHOD FOR MODULATION OF CELL PHENOTYPE
: FILE REFERENCE: 2048 84
: CURRENT APPLICATION NUMBER: US 09 420 060
: CURRENT FILING DATE: 1999-10-18
: NUMBER OF SEQ. IN NO.: 21
: SOFTWARE: Patent In Vol. 2.0
: SEQ. IN NO.: 8
: LENGTH: 420
: TYPE: PRI
: ORGANISM: Homo sapiens
US 09 420 060 8

```

Query Match	83.84%	Score: 95	DB: 18	Length: 428
Best Local Similarity	100.00%	Prod. No.: 3,40,06		
Matches: 19	Conservative: 0	Mismatches: 0	Indels: 0	Gaps: 0

07	4	ELSPRPSYRK	LNLS	SD	22
08	12	ELSPRPSYRK	LNLS	SD	140

```

RESULT: 8
PCT: 4502 27802 6
: Sequence 6: Application 10/1050227802
: GENERAL INFORMATION:
: APPLICANT: The Rockefeller University
: APPLICANT: The Rockefeller University
: TITLE OF INVENTION: METHOD FOR CLASSIFICATION OF ANTI-PSYCHOTIC DRUGS
: FILE REFERENCE: 1161 009 228
: CURRENT APPLICATION NUMBER: 101/1050227802
: CURRENT FILING DATE: 2002 09 03
: PCT# APPLICATION NUMBER: 60/416,338
: PCT# FILING DATE: 2001 08 31
: NUMBER OF SEQ. IN SEQSET: 8
: SOFTWARE: Patent in version 3.6
: SEQ. ID NO. 6
: LENGTH: 34
: TYPE: PRT
: ORGANISM: Homo sapiens
: 101 10502 27802 6

```

Query Match	83.89%	Score 93	105.1	Length 347
Best local Similarity	100.00%	Prod. No.	4,660	067
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0

07	4	E	L	S	P	R	S	Y	K	I	N	L	S	S	22
08	126	E	L	S	P	R	S	Y	K	I	N	L	S	S	144

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1 CORRESPONDENCE ADDRESS:  
 2 ADDRESSEE: Rothwell, Figg, Frost & Knorr  
 3 STREET: 1125 South 103rd Street, Suite 720  
 4 CITY: Omaha  
 5 STATE: Nebraska  
 6 COUNTRY: USA  
 7 ZIP: 68124  
 8  
 9 COMPUTER READABLE FORM:  
 10 MEDIUM TYPE: Floppy disk  
 11 COMPUTER: IBM PC compatible  
 12 OPERATING SYSTEM: PC-DOS/MS-DOS  
 13 SOFTWARE: Patent In Release #1.0, Version #1.00  
 14  
 15 CURRENT APPLICATION DATA:  
 16 APPLICATION NUMBER: US/08/881,800  
 17 FILING DATE:  
 18 CLASSIFICATION: 424  
 19 PRIOR APPLICATION DATA:  
 20 APPLICATION NUMBER: US/210,880  
 21 FILING DATE: 18 MAR 1994  
 22 ATTORNEY/AGENT INFORMATION:  
 23 NAME: Jondle, Robert J.  
 24 REGISTRATION NUMBER: 33,915  
 25 REFERENCE/PACKET NUMBER: N1241 006  
 26 TELECOMMUNICATION INFORMATION:  
 27 TELEPHONE: 402-398-9400  
 28 TELEFAX: 402-398-1983  
 29 INFORMATION FOR SEQ ID NO: 2:  
 30 SEQUENCE CHARACTERISTICS:  
 31 LENGTH: 341 amino acids  
 32 TYPE: amino acid  
 33 STRANDEDNESS:  
 34 TOPOLOGY: linear  
 35 MOLECULE TYPE: protein  
 36 ORIGINAL SOURCE:  
 37 ORGANISM: Homo sapiens  
 38

query Match 85.8%; Score 93; HB 12; Length 3417  
 best local Similarity 100.0%; Prod. No. 3.6e-06;  
 Matches 19; Conservative 0; Mismatches 0; Indels

QY	4	ELLKRRPSYRKILNLDSSD	22
DB	126	ELLKRRPSYRKILNLDSSD	144

```

1  RESULT 10
2  US 08 881-800A-2
3  Sequence 2, Application US/08881800A
4  GENERAL INFORMATION:
5  APPLICANT: HINTICHS, Steven H.
6  TITLE OF INVENTION: Methods and Compositions for Inhibiting
7  TITLE OF INVENTION: B ZIP Transcription Factor Pathways
8  NUMBER OF SEQUENCES: 12
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: Rothwell, Fiqq, Ernst & Kurz
11 STREET: 545 Thirteenth St., N.W., Suite 701 E.
12 CITY: Washington
13 STATE: DC
14 COUNTRY: USA
15 ZIP: 20004
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.00
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: 08-0881-800A
23 FILING DATE: 24-JUN-1997
24 CLASSIFICATION: 424
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 08-0881-800A
27 FILING DATE: 18-MAR-1994

```

```

; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
US 10 233-448-6

Query Match      83.8%; Score 93; DB 26; Length 341;
Best local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 4 EILSRPSPYRKIIINLSSD 22
   IIIIIIIIIIIIIIIIII
DB 126 EILSRPSPYRKIIINLSSD 144

RESULT 13
PCT-US00-28316-4
; Sequence 4, Application Pct/IUS0028316
; GENERAL INFORMATION:
; APPLICANT: Reusch, Jane E.
; APPLICANT: Klemm, Dwight J.
; TITLE OF INVENTION: METHOD FOR MODULATION OF CELL PHENOTYPE
; FILE REFERENCE: 2848-34-PCT
; CURRENT APPLICATION NUMBER: PCT/US99/28316
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/420,060
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Rattus rattus
PCT-US00-28316-4

Query Match      83.8%; Score 93; DB 1; Length 342;
Best local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 4 EILSRPSPYRKIIINLSSD 22
   IIIIIIIIIIIIIIIIII
DB 126 EILSRPSPYRKIIINLSSD 144

RESULT 14
US-09-420-060-4
; Sequence 4, Application US/09420060
; GENERAL INFORMATION:
; APPLICANT: Reusch, Jane E.
; APPLICANT: Klemm, Dwight J.
; TITLE OF INVENTION: METHOD FOR MODULATION OF CELL PHENOTYPE
; FILE REFERENCE: 2848-34
; CURRENT APPLICATION NUMBER: US2004/0450060
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-420-060-4

Query Match      83.8%; Score 93; DB 18; Length 342;
Best local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 4 EILSRPSPYRKIIINLSSD 22
   IIIIIIIIIIIIIIIIII
DB 126 EILSRPSPYRKIIINLSSD 144

RESULT 15
US-09-834-366-15787
; Sequence 15787, Application US/09834366

```

GENERAL INFORMATION:  
APPLICANT: Benjamin, Stephanie  
APPLICANT: Tanaka, Hiroaki  
APPLICANT: James Milne Edwards, Jean Baptiste  
APPLICANT: Robert, Steven H.  
APPLICANT: Giordano, Jean Yves  
TITLE OF INVENTION: ESTS and Encoded Human Proteins,  
FILE REFERENCE: 01 US2,PEG  
CURRENT APPLICATION NUMBER: US/09/834,366  
CURRENT FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: US 60/197,873  
PRIOR FILING DATE: 2000-04-18  
NUMBER OF SEQ ID NOS: 52153  
SOFTWARE: Patent.com  
SEQ ID NO: 15767  
LENGTH: 93  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: UNSUPE  
LOCATION: 80  
OTHER INFORMATION: Xaa Set, Thr  
US 09 834 366 15767

Query Match: 90.2% Score 89; 108 z2; Length 93;  
Best Local Similarity: 94.7% Pred. No. 3,1e-06;  
Matches: 48; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

27 4 EILSRRTSYVKIINDLSSD 22  
106 50 EILSRRTSYVKIINDLSSD 68

Search completed: January 2, 2003, 12:45:21  
Job time: 136 secs







RESULT 6  
PRT 0594 01668 1  
Sequence 1, Application US/09/0491368  
GENERAL INFORMATION:  
APPLICANT: Galk Institute Biological Studies  
TITLE OF INVENTION: PHOSPHOSPECIFIC  
TITLE OF INVENTION: TRANSFERRED IN FACTOR ANTIBODIES  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spectrolyt, Inc., 10000 S. 1st St., Suite 500  
STREET: 10000 S. 1st St., Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Patent In Release #1.0, Version  
SOFTWARE: #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 09/0491368  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D., John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: 4217  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619 455 5100  
TELEFAX: 619 455 5110  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURES:  
NAME/KEY: peptide  
LOCATION: 1-14  
PRT 0594 01668 1

Query Match  
Best Local Similarity: 100.0%; Score 50; DB 5; Length 14;  
Matches: 14; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 6 ELLSRKPTKINQ 14  
DB 1 ELLSRKPTKINQ 14

RESULT 7  
PRT 0926 01671 1  
Sequence 1, Application US/09/0491368  
Patent No. 6057117  
GENERAL INFORMATION:  
APPLICANT: Harrison, Stephen  
APPLICANT: Ring, David  
TITLE OF INVENTION: Identification and Use of Selective  
TITLE OF INVENTION: Inhibitors of Glycogen Synthase Kinases  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94608 2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 09/087832,567  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 1187,002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 924 2719  
TELEFAX: (510) 655 3542  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 09/09/262,971  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/832,567  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 1187,002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 924 2719  
TELEFAX: (510) 655 3542  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US 09-267 971-1

Query Match  
Best Local Similarity: 100.0%; Score 50; DB 3; Length 17;  
Matches: 10; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 ELLSRRPSYR 13  
DB 8 ELLSRRPSYR 17

RESULT 7  
US-08-832 567-1  
Sequence 1, Application US/08832567  
Patent No. 6057286  
GENERAL INFORMATION:  
APPLICANT: Harrison, Stephen  
APPLICANT: Ring, David  
TITLE OF INVENTION: Identification and Use of Selective  
TITLE OF INVENTION: Inhibitors of Glycogen Synthase Kinases  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94608 2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/087832,567  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 1187,002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 924 2719  
TELEFAX: (510) 655 3542  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
US-08-836-038-1

Query Match 45.0%; Score 50; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRKPSYR 13
Db 8 EILSRKPSYR 17

RESULT 8
US-09-336-038-2
; Sequence 2; Application US/09336038
; Patent No. 6417185
; GENERAL INFORMATION:
; APPLICANT: Goff, Dane
; APPLICANT: Harrison, Steven
; APPLICANT: Nuss, John
; APPLICANT: Rhee, David R.
; APPLICANT: Zhou, Xiaohai A.
; TITLE OF INVENTION: Inhibitors of Glycogen Synthase Kinase 3
; FILE REFERENCE: 1443.093
; CURRENT APPLICATION NUMBER: 05/09/336,038
; CURRENT FILING DATE: 1999-06-19
; EARLIER APPLICATION NUMBER: 60/089,978
; EARLIER FILING DATE: 1998-06-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRI
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: SGGG-linked CPEP peptide; Ser in position 15 must be phosphorylated
US-09-336-038-2

Query Match 45.0%; Score 50; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRKPSYR 13
Db 8 EILSRKPSYR 17

RESULT 9
US-08-319-866-2
; Sequence 2; Application US/08319866
; Patent No. 5929227
; GENERAL INFORMATION:
; APPLICANT: Tully, Timothy P.
; APPLICANT: Yin, Terry C.
; APPLICANT: Replinski, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENUS
; NUMBER OF SEQUENCES: 2;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 05/09/319,866
; FILING DATE: 7-OCT-1994

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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-319-866-2

Query Match 45.0%; Score 50; DB 2; Length 360;
Best Local Similarity 60.0%; Pred. No. 3;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LSKRPSSYRKILNLS 20
Db 226 LSKRPSSYRKILNLS 240

RESULT 10
US-08-946-994-17
; Sequence 17; Application US/08946994
; Patent No. 6210654
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvenoinen, Ollie
; APPLICANT: Withuhn, Bruce A.
; APPLICANT: Quille, Frederick W.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal
; TITLE OF INVENTION: Transduction
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 05/09/946,994
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 05/09/665,574
; FILING DATE: 18-JUN-1996
; APPLICATION NUMBER: 08/282,012
; FILING DATE: 29-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/997,997
; FILING DATE: 29-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/118,968
; FILING DATE: 09-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600

```



TELEFAX: (202) 471-2540  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1098 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-665-574-16  
Query Match 42.3%; Score 47; DB 4; Length 1098;  
Best Local Similarity 69.2%; Pred. No. 42;  
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
27 8 RPPSYRKILNDLS 20  
1111111111  
DB 761 RPSFRATILRLN 774  
PL311 11  
US-08-665-574-16  
Sequence 16, Application US/086655740  
Patent No. 6166545  
GENERAL INFORMATION:  
APPLICANT: Thilo, James N.  
APPLICANT: Stizenbiller, Willie  
APPLICANT: Withuhn, Bruce A.  
TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine  
TITLE OF INVENTION: Signal Transduction  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 900  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/282,012  
FILING DATE: 18 JUN 1996  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/282,012  
FILING DATE: 29 JUL 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/282,007  
FILING DATE: 29 JUL 1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/118,968  
FILING DATE: 09 SEP 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Butalsky, Lawrence B.  
REGISTRATION NUMBER: 467086  
REFERENCE/WORKS NUMBER: 08/282,012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 471-2540  
TELEFAX: (202) 471-2540  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1099 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-665-574-16

Query Match 42.3%; Score 47; DB 4; Length 1099;  
Best Local Similarity 69.2%; Pred. No. 42;  
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 RPPSYRKILNDLS 20  
1111111111  
DB 761 RPSFRATILRLN 774  
RESULT 12  
US-08-657-598-11  
Sequence 11, Application US/08657598  
Patent No. 5705625  
GENERAL INFORMATION:  
APPLICANT: Civin, Curt L.  
APPLICANT: Small, Donald  
TITLE OF INVENTION: REVEL PROTEIN TYROSINE KINASE, JAK  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.40  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/097497, 598  
FILING DATE: 15 DEC 1994  
CLASSIFICATION: 430  
ATTORNEY/AGENT INFORMATION:  
NAME: Bailo, Lisa A.  
REGISTRATION NUMBER: 48,347  
REFERENCE/WORKS NUMBER: 072057043001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1100 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-657-598-11

Query Match 42.3%; Score 47; DB 1; Length 1100;  
Best Local Similarity 69.2%; Pred. No. 42;  
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 RPPSYRKILNDLS 20  
1111111111  
DB 762 RPSFRATILRLN 774  
RESULT 13  
US-09-004-289-11  
Sequence 11, Application US/09004289  
Patent No. 5916792  
GENERAL INFORMATION:  
APPLICANT: Civin, Curt L.  
APPLICANT: Small, Donald  
TITLE OF INVENTION: REVEL PROTEIN TYROSINE KINASE, JAK  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/004,289
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/357,598
: FILING DATE: 15-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Baile, Lisa A.
: REGISTRATION NUMBER: 38,347
: REFERENCE/EXCIT NUMBER: 07265/033W01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678 5070
: TELEFAX: 619/678-5099
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1100 amino acids
: TYPE: amino acid
: STRANDEDNESS: No. 5916792 Relevant
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-004-289-11

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```

Query Match 42.3% Score 47 DB 2 Length 1100
Best Local Similarity 69.2% Pred. No. 32
Matches 9 Conservative 2 Mismatches 2 Indels 0 Gaps 0

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```

QY 8 RKPSYRKILNDLS 20
   ||||| || |||
Db 762 RRPSPRAILRLN 774

```

RESULT 14

```

PCT-US95-16435-11
: Sequence 1: Application PCT/US95/03164
: GENERAL INFORMATION:
: APPLICANT: The Johns Hopkins University School of Medicine
: TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 425 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/03164
: FILING DATE: 15 DEC 1995
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Baile, Lisa A.
: REGISTRATION NUMBER: 38,347
: REFERENCE/EXCIT NUMBER: 07265/033W01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678 5070
: TELEFAX: 619/678 5099
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1100 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US95-16435-11

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```

Query Match 42.3% Score 47 DB 5 Length 1100
Best Local Similarity 69.2% Pred. No. 32
Matches 9 Conservative 2 Mismatches 2 Indels 0 Gaps 0

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```

QY 8 RKPSYRKILNDLS 20
   ||||| || |||
Db 762 RRPSPRAILRLN 774

```

RESULT 15

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PCT-US95-08354A-2
: Sequence 2: Application PCT/US95/08354A
: GENERAL INFORMATION:
: APPLICANT: Temple University - Of The
: APPLICANT: Commonwealth System of Higher Education
: TITLE OF INVENTION: JAK2 PROTEIN TYROSINE
: TITLE OF INVENTION: KINASE AND DNA ENCODING THE SAME
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seidel, Gonda, Lavorata
: ADDRESSEE: & Monaco, P.C.
: STREET: Suite 1800, Two Penn Center
: CITY: Philadelphia
: STATE: Pennsylvania
: COUNTRY: U.S.A.
: ZIP: 19102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/08354A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08,322,468
: FILING DATE: 8 July 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Monaco, Daniel A.
: REGISTRATION NUMBER: 30,480
: REFERENCE/EXCIT NUMBER: 6056-203 PC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-8383
: TELEFAX: (215) 568-5549
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1299 amino acids
: TYPE: amino acid
: STRANDEDNESS: single stranded
: TOPOLOGY: linear
: PCT-US95-08354A-2

```

```

Query Match 42.3% Score 47 DB 5 Length 1299
Best Local Similarity 69.2% Pred. No. 38
Matches 9 Conservative 2 Mismatches 2 Indels 0 Gaps 0

```

```

QY 8 RKPSYRKILNDLS 20
   ||||| || |||
Db 977 RRPSPRAILRLN 989

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Search completed: January 2, 2003, 12:29:45  
 Job time: 13 secs

GenScore version 5.1.1.3  
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AM protein protein search, using sw model

Run on: January 2, 2003, 12:29:25, Search time 7.5 seconds  
(without alignments)  
58,118 Million cell updates/sec

Files: us-09-786-317-1  
Perfect score: 111  
Sequence: 1 USSE11SRPSPYRKILNLSSTP 23

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum hit seq length: 9  
Maximum hit seq length: 269999999

Post processing: Minimum Match 9%  
Maximum Match 100%  
Listing first 45 summaries

Database:		Published Applications_AA:*	
1	us-09-786-317-1	us-09-786-317-1	us-09-786-317-1
2	us-09-786-317-1	us-09-786-317-1	us-09-786-317-1
3	us-09-786-317-1	us-09-786-317-1	us-09-786-317-1
4	us-09-786-317-1	us-09-786-317-1	us-09-786-317-1
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9	us-09-786-317-1	us-09-786-317-1	us-09-786-317-1
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11	us-09-786-317-1	us-09-786-317-1	us-09-786-317-1
12	us-09-786-317-1	us-09-786-317-1	us-09-786-317-1
13	us-09-786-317-1	us-09-786-317-1	us-09-786-317-1
14	us-09-786-317-1	us-09-786-317-1	us-09-786-317-1

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	45.3	13	10	us-09-971-118 7
2	50	45.3	13	10	us-09-951-902 1
3	50	45.3	13	10	us-09-951-902-2
4	47	42.3	13	10	us-09-951-902-5
5	45	40.5	9	10	us-09-951-902 3
6	45	40.5	9	10	us-09-951-902 12
7	44	39.6	289	10	us-09-764-864-984
8	44	39.6	504	9	us-10-114-893-67
9	44	39.6	1124	10	us-09-771-161A 199
10	43	38.7	577	10	us-09-815-242 11305
11	43	38.7	915	10	us-09-817-514A 6
12	43	38.7	1131	10	us-09-801-368 72
13	42	37.8	8	9	us-10-014-485A 115
14	42	37.8	9	10	us-09-951-902 6
15	42	37.8	44	10	us-09-864-761 47295
16	41	36.9	9	10	us-09-951-902 4
17	41	36.9	140	10	us-09-764-864 1447
18	41	36.9	277	10	us-09-927-738 1
19	41	36.9	377	10	us-09-925-406-1180

20	41	36.9	940	9	us-09-811-088 11
21	40	36.0	308	10	us-09-815-242 5150
22	40	36.0	419	9	us-09-738-626 5297
23	40	36.0	423	9	us-09-712-363 248
24	40	36.0	566	10	us-09-925-297 668
25	40	36.0	712	10	us-09-864-761 3450
26	39.5	35.6	150	9	us-09-860-670 128
27	39.5	35.6	936	9	us-10-060-230-19
28	39.5	35.6	906	9	us-10-060-230 20
29	39.5	35.6	906	9	us-10-060-230-21
30	39.5	35.6	906	9	us-10-060-230 22
31	39.5	35.6	1220	10	us-09-801-368-332
32	39.5	35.6	3056	8	us-08-984 090 2
33	39	35.1	236	9	us-09-764 868-870
34	39	35.1	1129	9	us-10-024 623-14
35	39	35.1	4861	10	us-09-919 497 70
36	38.5	34.7	455	10	us-09-757 982 5
37	38.5	34.7	888	10	us-09-864-761 42969
38	38.5	34.7	1285	10	us-09-982 091A 2
39	38	34.2	60	10	us-09-864 761 47716
40	38	34.2	114	9	us-09-808 602 111
41	38	34.2	193	9	us-09-738 626 5547
42	38	34.2	344	10	us-09-815-242-1158 3
43	38	34.2	367	10	us-09-731-872 395
44	38	34.2	367	10	us-09-731 872 403
45	38	34.2	1230	10	us-09-727-384-8

ALIGNMENTS

RESULT 1  
us-09-971-118 7  
Sequence 3, Alignment 1, us-09-971-118  
Patent No. US20020123056A1  
GENERAL INFORMATION:  
APPLICANT: DELANEY, ALLEN  
APPLICANT: VOGARATHAN, INILAKATHAN  
TITLE OF INVENTION: SEED AND ITS USES  
FILE NUMBER: 2001-09-20  
CURRENT APPLICATION NUMBER: 60/237,419  
PRIORITY FILING DATE: 2001-09-20  
PRIORITY FILING DATE: 2001-09-20  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID No 7  
LENGTH: 14  
TYPE: PRI  
ORGANISM: Homo sapiens  
us-09-971-118-7

Query Match 45.0% Score 50; DB ID: Length 13;  
Best Local Similarity 100.0%; Prod. No. 0.031;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELSRRRPSYR 13  
DB 4 ELSRRRPSYR 13

RESULT 2  
us-09-951-902-1  
Sequence 1, Application US/09951902  
Patent No. US20020147146A1  
GENERAL INFORMATION:  
APPLICANT: ELIAR FINKELMAN, Basil  
TITLE OF INVENTION: GLYCOSYL SYNTHASE INHIBITORS  
FILE REFERENCE: ELIAR-FINK 1.1B  
CURRENT APPLICATION NUMBER: US/09/951,902  
CURRENT FILING DATE: 2001 09 14

```
; PRIOR APPLICATION NUMBER: US/09951902
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/206,115
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/174,308
; PRIOR FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: Ser residue 11 is phosphorylated.
US-09-951-902-1
```

```
Query Match          45.0%; Score 50; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 EILSRPPSYR 13
      ||| ||| |||
Db       4 EILSRPPSYR 13
```

## RESULT 3

```
US-09-951-902-2
; Sequence 2: Application US/09951902
; Patent No. US20020147146A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ELDAR-FINKELMAN, Hagit
; TITLE OF INVENTION: GLYCOGEN SYNTHASE KINASE-3 INHIBITORS
; FILE REFERENCE: ELDAR-FINK=1.1B
; CURRENT APPLICATION NUMBER: US/09951902
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/174,308
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: 60/206,115
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/174,308
; PRIOR FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-951-902-2
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```
Query Match          45.0%; Score 50; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 EILSRPPSYR 13
      ||| ||| |||
Db       4 EILSRPPSYR 13
```

## RESULT 4

```
US-09-951-902-5
; Sequence 5: Application US/09951902
; Patent No. US20020147146A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ELDAR-FINKELMAN, Hagit
; TITLE OF INVENTION: GLYCOGEN SYNTHASE KINASE-3 INHIBITORS
; FILE REFERENCE: ELDAR-FINK=1.1B
; CURRENT APPLICATION NUMBER: US/09951902
; CURRENT FILING DATE: 2001-09-14
```

```
; PRIOR APPLICATION NUMBER: US/09951902
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/206,115
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/174,308
; PRIOR FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: Ser residue 11 is phosphorylated.
US-09-951-902-5
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Query Match          42.3%; Score 47; DB 10; Length 13;
Best Local Similarity 90.0%; Pred. No. 0.093;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 EILSRPPSYR 13
      ||| ||| |||
Db       4 EILSRPPSYR 13
```

## RESULT 5

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US-09-951-902-3
; Sequence 3: Application US/09951902
; Patent No. US20020147146A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ELDAR-FINKELMAN, Hagit
; TITLE OF INVENTION: GLYCOGEN SYNTHASE KINASE-3 INHIBITORS
; FILE REFERENCE: ELDAR-FINK=1.1B
; CURRENT APPLICATION NUMBER: US/09951902
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/174,308
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: 60/206,115
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/174,308
; PRIOR FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: Ser residue 7 is phosphorylated.
US-09-951-902-3
```

```
Query Match          40.5%; Score 45; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 ILSRRPPSYR 13
      ||| ||| |||
Db       1 ILSRRPPSYR 9
```

## RESULT 6

```
US-09-951-902-12
; Sequence 12: Application US/09951902
; Patent No. US20020147146A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ELDAR-FINKELMAN, Hagit
; TITLE OF INVENTION: GLYCOGEN SYNTHASE KINASE-3 INHIBITORS
```

; FILE REFERENCE: ELIAR FIRM 1.1B  
 ; CURRENT APPLICATION NUMBER: 09/09764864  
 ; CURRENT FILING DATE: 2001 01 13  
 ; PRIOR APPLICATION NUMBER: 09/09764864/0.12  
 ; PRIOR FILING DATE: 2001 01 13  
 ; PRIOR APPLICATION NUMBER: 09/206115  
 ; PRIOR FILING DATE: 2000 05 22  
 ; PRIOR APPLICATION NUMBER: 09/174308  
 ; PRIOR FILING DATE: 2000 01 03  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Patent In Version 3.1  
 ; SEQ ID NO 12  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 US 09 951 902 12

Query Match 40.6% Score 45; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9,86004;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 USRRPSYPK 13  
 I I I I I I I

DB 1 USRRPSYPK 9

RESULT 7

US 09 764 864 984  
 ; Sequence 984, Application US/09764864  
 ; Patent No. US20020132753A1

; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: P1223  
 ; CURRENT APPLICATION NUMBER: US/09764864  
 ; CURRENT FILING DATE: 2001 01 17  
 ; Prior application data removed consult PAM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 1792  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 984  
 ; LENGTH: 289  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US 09 764 864 984

Query Match 49.6% Score 44; DB 10; Length 289;  
 Best Local Similarity 65.0%; Pred. No. 10;  
 Matches 11; Conservative 1; Mismatches 8; Indels 8; Gaps 0;

QY 1 USSELSEKREYKRIINLS 20  
 I I I I I I I I I I

DB 228 IQASLLPAYSPLNLS 247

RESULT 8

US 10 114 893 67  
 ; Sequence 67, Application US/10114893  
 ; Publication No. US2002019367A1

; GENERAL INFORMATION:  
 ; APPLICANT: Jacobs, Kenneth  
 ; APPLICANT: McCoy, John M.  
 ; APPLICANT: LaValley, Edward R.  
 ; APPLICANT: Collins, Emily, Lisa A.  
 ; APPLICANT: Evans, Cheryl  
 ; APPLICANT: Morberg, David  
 ; APPLICANT: Treacy, Maurice  
 ; APPLICANT: Bowman, Michael R.  
 ; APPLICANT: Spaulding, Vikki  
 ; APPLICANT: Carlin Buckett, McKenough  
 ; APPLICANT: Koolhaas, Kerry S.  
 ; APPLICANT: Genetics Institute, Inc.

; TITLE OF INVENTION: STACKED PROTEINS AND POLYMERIZED FILLS INCLUDING THEM  
 ; FILE REFERENCE: US 09/09764864  
 ; CURRENT APPLICATION NUMBER: 09/206114, 893  
 ; CURRENT FILING DATE: 2002-04-02  
 ; EARLIER APPLICATION NUMBER: 09/206114, 222  
 ; EARLIER FILING DATE: 1999 10-06  
 ; NUMBER OF SEQ ID NOS: 321  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 67  
 ; LENGTH: 504  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-114-893-67

Query Match 49.6% Score 44; DB 9; Length 504;  
 Best Local Similarity 47.4%; Pred. No. 20;  
 Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 5 ILSRPSYRKIIINLS 23  
 I I I I I I I I I I

DB 276 IESRRPAYSPLNLS 288

RESULT 9

US-09-771-161A-199  
 ; Sequence 199, Application US/09771161A  
 ; Patent No. US2002010811A1

; GENERAL INFORMATION:  
 ; APPLICANT: Levine, et al.  
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
 ; FILE REFERENCE: 802620 200511  
 ; CURRENT APPLICATION NUMBER: US/09771161A  
 ; CURRENT FILING DATE: 2001 01-26  
 ; PRIOR APPLICATION NUMBER: 09/724, 676  
 ; PRIOR FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: 136776  
 ; PRIOR FILING DATE: 2000 06 15  
 ; PRIOR APPLICATION NUMBER: 135619  
 ; PRIOR FILING DATE: 2000-04 12  
 ; NUMBER OF SEQ ID NOS: 273  
 ; SOFTWARE: Patent In Version 3.0  
 ; SEQ ID NO 199  
 ; LENGTH: 1124  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09 771 161A 199

Query Match 49.6% Score 44; DB 10; Length 1124;  
 Best Local Similarity 50.0%; Pred. No. 90;  
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 5 IESRRPAYSPLNLS 21  
 I I I I I I I I I I

DB 766 QIESRRPAYSPLNLS 779

RESULT 10

US-09 815 242 11305  
 ; Sequence 11305, Application US/09815242  
 ; Patent No. US20020061569A1

; GENERAL INFORMATION:  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Karl L.  
 ; APPLICANT: Zyskind, Judith W.  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John B.  
 ; APPLICANT: Carr, Grant J.  
 ; APPLICANT: Yamamoto, Robert L.  
 ; APPLICANT: Xu, H. Howard  
 ; TITLE OF INVENTION: Identification of Essential Gaps in  
 ; FILE REFERENCE: ELIAR.F11A  
 ; CURRENT APPLICATION NUMBER: US/09/815, 242

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; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,818
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,331
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11305
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11305
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```
Query Match 38.7%; Score 43; DB 10; Length 577;
Best Local Similarity 42.1%; Pred. No. 33;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 4 EILSRPSPSYRKILNLSQ 22
      | | | | | | | | | |
Db 173 REINIQSAYKFTISLGLD 191
```

```
RESULT 11
US-09-817-514A-6
; Sequence 6; Application US/09817514A
; Patent No. US20020078478A1
; GENERAL INFORMATION:
; APPLICANT: French-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTOBACULUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 6
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Photobaculus luminescens
US-09-817-514A-6
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```
Query Match 38.7%; Score 43; DB 10; Length 915;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 5 ILSRKPSYRKILNOL 19
      | | | | | | | | | |
Db 300 IITRPISDAKVIQDL 314
```

```
RESULT 12
US-09-801-368-72
; Sequence 72; Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
```

```
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: R. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for determining secondary metabolite production in fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US 09/93,07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
; LENGTH: 1131
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US 09 801 368 72
```

```
Query Match 39.7%; Score 43; DB 10; Length 1131;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 TSSEILSRPSPSYRKILN 18
      | | | | | | | | | |
Db 997 SSSEIQANYDKYIKVLND 1014
```

```
RESULT 13
US-10-014-485A-115
; Sequence 115; Application US/10014485A
; Patent No. US20020168684A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: GOMB, Michael J.
; APPLICANT: ZHANG, Hui
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: PROTECTION OF MOTIF SPECIFIC AND CONTEXT INDEPENDENT ANTIBODIES
; FILE REFERENCE: CST-138 CIP2
; CURRENT APPLICATION NUMBER: US/10/014,485A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: US 63/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 115
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: PHOSPHORYLATION: serine at position 5 is phosphorylated
US-10-014-485A-115
```

```
Query Match 37.8%; Score 42; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 9,80-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 SRSPSYRK 14
      | | | | | | | |
Db 1 SRSPSYRK 8
```

Result 14  
US 09 751 902 6  
Sequence 6, Application US/09/051902  
Patent No. US2002/0147146A1  
GENERAL INFORMATION:  
APPLICANT: ELLAR FINKELMAN, HAITI  
TITLE OF INVENTION: GLYCERIN SYNTHASE KINASE 3 INHIBITORS  
FILE REFERRED: ELLAR FINK 1-13  
CURRENT APPLICATION NUMBER: 09/09/951,902  
CURRENT FILING DATE: 2001 09 14  
PRIOR APPLICATION NUMBER: PCT/US01/00129  
PRIOR FILING DATE: 2001 01 03  
PRIOR APPLICATION NUMBER: 60/266,115  
PRIOR FILING DATE: 2000 05 22  
PRIOR APPLICATION NUMBER: 60/174,408  
PRIOR FILING DATE: 2000 01 03  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 4.1  
SEQ ID NO 6  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
NAME/KEY: misc feature  
Location: (9)...(8)  
OTHER INFORMATION: Ser residue 8 is phosphorylated.  
US 09 951 902 6

Query Match 37.8% Score 42; 10 16; Length 9;  
Best Local Similarity 88.9% Pred. No. 9,80,004;  
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

27 4 ELLARFINK 12  
1111111  
Db 1 ELLARFINK 9

Result 15  
US 09 864 761 4/295  
Sequence 4/295, Application US/99/864761  
Patent No. US2002/0048766A1  
GENERAL INFORMATION:  
APPLICANT: Penn. Shattou G.  
APPLICANT: Bank, David R.  
APPLICANT: Bank, David R.  
APPLICANT: Chong, Weischedel  
TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEOTIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Assembly X 1  
CURRENT APPLICATION NUMBER: 99/09/864,761  
CURRENT FILING DATE: 2001 05 23  
PRIOR APPLICATION NUMBER: US 60/189,312  
PRIOR FILING DATE: 2000 02 04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000 05 26  
PRIOR APPLICATION NUMBER: US 09/632,356  
PRIOR FILING DATE: 2000 08 03  
PRIOR APPLICATION NUMBER: BR 2426336  
PRIOR FILING DATE: 2000 10 04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000 09 27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001 01 40  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001 01 40  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001 01 40  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001 01 40  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001 01 40  
PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001 01 40  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001 01 40  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001 01 40  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001 01 40  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001 01 40  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000 09 21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000 06 30  
PRIOR APPLICATION NUMBER: US 09/174,203  
PRIOR FILING DATE: 2001 01 29  
NUMBER OF SEQ ID NOS: 4917  
SOFTWARE: Anomax Sequence List for Routine vers. 1.1  
SEQ ID NO 47295  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC000120.1  
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL 0.47  
OTHER INFORMATION: EXPRESSED IN ADIP3 LIVER, SIGNAL 0.41  
OTHER INFORMATION: SWISSPROT HIT: Q1625, EVALUOE 9,500 01  
OTHER INFORMATION: EST\_HUMAN HIT: M62430.1, EVALUOE 2,000 12  
US-09-864-761-47295

Query Match 37.8% Score 42; 10 16; Length 44  
Best Local Similarity 59.0% Pred. No. 2,14;  
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 SE11SRPFSYKRIINLSSD 22  
11111111111111111111  
Db 19 SE11SRPFSYKRIINLSSD 48

Search completed: January 2, 2003, 12:00:11  
Job time : 7.5 secs





Genome version 6.1.3  
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W protein protein search using sw model

Run on: January 2, 2003, 12:26:41 : Search time 31 seconds  
(without alignments)  
98,863 Million cell updates/sec

Index: US-09-786-317-1

Perfect score: 111

Sequence: 1 TSSSETLSPRESEYKTLNTLSSD1\_23

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Search: 90847 seqs, 100250620 residues

Total number of hits satisfying chosen parameters: 908470

Maximum DB seq length: 9

Maximum DB seq length: 20000000

Post processing: Minimum Match 0%

Maximum Match 100%

Using first 45 summaries

Database: A Geneseq 101021*			
1	230000000	100000000	100000000
2	230000000	100000000	100000000
3	230000000	100000000	100000000
4	230000000	100000000	100000000
5	230000000	100000000	100000000
6	230000000	100000000	100000000
7	230000000	100000000	100000000
8	230000000	100000000	100000000
9	230000000	100000000	100000000
10	230000000	100000000	100000000
11	230000000	100000000	100000000
12	230000000	100000000	100000000
13	230000000	100000000	100000000
14	230000000	100000000	100000000
15	230000000	100000000	100000000
16	230000000	100000000	100000000
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19	230000000	100000000	100000000
20	230000000	100000000	100000000
21	230000000	100000000	100000000
22	230000000	100000000	100000000
23	230000000	100000000	100000000

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Match	Length	DB	Description
1	111	100.0	24	23	AA081935
2	93	83.8	60	22	AA073033
3	93	83.8	327	11	AA066111
4	93	83.8	327	22	AA060652
5	93	83.8	327	22	AA073231
6	93	83.8	329	22	AA060655
7	93	83.8	342	22	AA060653
8	79	71.2	22	22	AA065587
9	76	68.5	24	22	AA070221
10	76	68.5	22	22	AA065586

11	75	67.6	271	22	AA060644
12	70	63.1	14	15	AA060491
13	62	55.9	12	22	AA070222
14	59	53.2	12	22	AA070223
15	57	51.4	22	22	AA065585
16	55	49.5	11	21	AA085174
17	55	49.5	11	22	AA099792
18	55	49.5	11	22	AA070447
19	55	49.5	14	22	AA065261
20	51	45.9	369	22	AA062122
21	50	45.0	13	22	AA064303
22	50	45.0	13	22	AA064304
23	50	45.0	13	22	AA066999
24	50	45.0	13	23	AA022770
25	50	45.0	13	23	AA067614
26	50	45.0	13	23	AA080050
27	50	45.0	17	21	AA091047
28	50	45.0	17	21	AA091049
29	50	45.0	359	22	AA062058
30	50	45.0	360	17	AA091294
31	49	44.1	706	23	AA073675
32	47	42.3	13	22	AA064302
33	47	42.3	100	23	AA075290
34	47	42.3	577	18	AA020634
35	47	42.3	1098	22	AA060358
36	47	42.3	1099	21	AA065715
37	47	42.3	1293	17	AA085560
38	47	42.3	2440	18	AA020828
39	46.5	41.9	364	22	AA031304
40	46.5	41.9	452	22	AA064533
41	46	41.4	107	22	AA065354
42	46	41.4	367	22	AA071497
43	46	41.4	723	23	AA023480
44	45	40.5	1	22	AA065353
45	45	40.5	120	22	AA064717

ALIGNMENTS

RESULT 1

AA081935

15 AA081935 standard, peptide, 27 AA.

XX AA081935;

XX 30-100-2000 (first entry)

XX 3538 phosphorylation regions

XX Phosphorylation region: monitor protein: inhibited identification

XX Protein phosphorylation measurement: CREB.

XX Unidentified.

XX W0200014108 AT.

XX 36 MAK 2000.

XX 02 SEP 1999; 99W01J04769.

XX 02 SEP 1998; 98JP 0248861.

XX (AUSC) GEN1 ADVANCED SCI & TECHNOLOGY INCORPORATED

XX Hagiwara M, Imouye S, Naito Y.

XX W01, 2000) 256938/22.

XX Phosphorylation monitor protein for convenient measurement of

XX phosphorylation of protein: applicable for in vitro determination

XX without needing radioisotope and in studying phosphorylation reaction

XX and screening compounds

XX  
PS Claim 5; Page 38; 45pp; Japanese  
XX  
CC This sequence represents a cAMP phosphorylation region.  
CC The invention relates to a monitor protein (1) for measuring  
CC phosphorylation of a protein. (1) comprises a protein containing a  
CC phosphorylation region and a characteristically variable region, where  
CC characteristics vary due to a change in the stereostructure. It is  
CC conveniently applicable for use in in vivo determination without needing  
CC radioisotopes. (1) is useful for the measurement of phosphorylation of  
CC protein, and for in vivo determination without needing radioisotopes  
CC e.g. in studying phosphorylation reaction and screening kinases and  
CC promoters and inhibitors of phosphorylation.  
XX  
SQ Sequence 23 AA.  
  
Query Match 100.0%; Score 111; DP 21; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.5e 10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TSSEILSRPPSYRKILNDLSSD 23  
DB 1 TSSEILSRPPSYRKILNDLSSD 23  
  
RESULT 2  
AAB73093  
ID AAB73093 standard; protein; 60 AA.  
XX  
AC AAB73093;  
DI 05-JUN-2001 (first entry)  
XX  
DE Rheumatoid arthritis treatment related protein #2.  
KW Mouse; rheumatoid arthritis; CREB; CBP;  
KW articular synovial cell proliferation inhibitor.  
XX  
OS Mus sp.  
XX  
PN W0200119489-A1.  
XX  
PB 22 MAR-2001.  
XX  
PF 11-SEP-2000; 2000W0 JP06180.  
XX  
PR 10-SEP-1999; 99JP-0256872.  
XX  
PA (CYBER ) UNIV ST MARIANNA SCHOOL MEDICINE.  
PA (SANT ) SANTEN PHARM CO LTD.  
XX  
PI Nakajima T, Nishioka K;  
XX  
DR WPI: 2001-244702/25.  
XX  
PT Remedies for rheumatoid arthritis and articular synovial cell  
PT proliferation inhibitors, comprises phosphorylated cyclic adenosine  
PT monophosphate response element binding protein recognition region of  
PT CBP including fused proteins -  
XX  
PS Disclosure; Page 22; 28pp; Japanese.  
XX  
SQ The present invention provides a remedy for rheumatoid arthritis,  
SQ comprising the phosphorylated cyclic adenosine monophosphate response element  
SQ binding protein (CREB) recognition region of CBP which is a phosphorylated  
SQ CREB coactivator. This is useful in the inhibition of proliferation of  
SQ articular synovial cells, thereby treating rheumatoid arthritis.  
XX  
SQ Sequence 60 AA;  
  
Query Match 92.8%; Score 93; DP 22; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPPSYRKILNDLSSD 22  
DB 24 EILSRPPSYRKILNDLSSD 44  
  
RESULT 4  
AAR06611  
ID AAR06611 standard; protein; 327 AA.  
XX  
AC AAR06611;  
DI 23-OCT-1990 (first entry)  
XX  
DE cAMP responsive transcription enhancer binding protein (CREB).  
KW cAMP responsive transcription enhancer binding protein; CREB;  
KW cAMP-response element; CRE; ds.  
XX  
OS Homo sapiens.  
XX  
PN W09005745-A.  
XX  
PD 31-MAY-1990.  
XX  
PF 20-NOV-1989; 89W0-0005234.  
XX  
PR 18-NOV-1988; 88US-0272980.  
XX  
PA (GEHO-) GEN HOSPITAL CORP.  
XX  
PI Habener JF, Hoefler JP;  
XX  
DR WPI: 1990 193436/25.  
DR N PSDB; AA004780.  
XX  
PT cAMP-responsive transcription enhancer binding protein (creb) -  
PT positively or negatively regulates expression of heterologous  
PT gene operably linked to it.  
XX  
PS Claim 1; Fig 1A-D; 32pp; English.  
XX  
CC CREB activates expression of eukaryotic genes in the presence of  
CC cAMP, it may thus be operably linked to a required heterologous  
CC gene and used to control its expression.  
XX  
SQ Sequence 327 AA;  
  
Query Match 83.9%; Score 94; DP 11; Length 327;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 EILSRPPSYRKILNDLSSD 22  
DB 112 EILSRPPSYRKILNDLSSD 130  
  
RESULT 4  
AAE00652  
ID AAE00652 standard; protein; 327 AA.  
XX  
AC AAE00652;  
DI 02-JUL-2001 (first entry)  
XX  
DE Human cyclic AMP responsive element binding protein (CREB).  
XX  
KW Human, cyclic adenosine mono phosphate, cell phenotype modulatory; CREB;  
KW cAMP responsive element binding protein; antidiabetic; cytostatic;  
KW neuroprotective; neotropic; osteoplastic; antiarthritic; antiapical;  
KW antiatherosclerotic; vasotropic; vasoprotective; antidepressant;  
KW cardiac; hypotensive; obesity; cardiovascular disease; cardiomyopathy;  
KW angiostatic; tumor; failure; cancer; cancer; cancer; hypertension;

KW acute myocardial infarction; stroke; peripheral vascular disease;  
KW post-angioplasty restenosis; heart failure; neurodegenerative disease;  
KW Alzheimer's disease; Parkinson's disease; spinal transection;  
KW acute neuronal ischemia; tumour neovascularisation;  
XX  
CS Homo sapiens  
XX  
XX  
FH Key location/positions  
FH domain 191...147  
FH /label Kinase-inducible domain  
FH /note "Important for activation and biological  
FH activation of wild type CREB"  
FH 260...294  
FH /note "C-terminal basic region important for wrapping  
FH around the DNA and therefore for DNA binding"  
FH domain 294...327  
FH /label "Leucine zipper domain"  
FH /note "Important for DNA binding"  
FH Missed difference 326...327  
FH /note "Encoded by 17A"  
XX  
FN W2200129962 AA2  
XX  
XX 27 APR 2001  
XX  
XX 12 OCT 2000; 2000WHO US28316;  
XX  
XX 18 OCT 1999; 99US 0420669;  
XX  
XX (BYE ) UNIV TECHNOLOGY CORP.  
FA (NAJE ) NAI JEWISH MEDICAL & RES CENT.  
FA (US555 ) US DEPT VETERANS AFFAIRS.  
XX  
XX Reusch JE. KGenm 1d1;  
XX  
XX WPI: 2001 200991/30.  
XX N PSDB: AAE00658.  
XX  
FH Modulating cell phenotype in a patient having or risk of developing a  
FH disease/condition linked with dysregulation of cellular phenotype,  
FH comprises administering nucleic acid encoding cyclic AMP responsive  
FH element binding protein  
XX  
XX Claim 5; Page 133-134; 156pp; English.  
XX  
XX The present sequence is human cyclic adenosine mono phosphate (cAMP)  
XX responsive element binding protein (CREB) which is a transcription  
XX factor necessary and sufficient to induce a modulation in cell  
XX phenotype and to induce cell differentiation in many cells.  
XX The patient discloses a method for modulating the phenotype of a target  
XX cell population in a patient who has or is at risk of developing a  
XX disease or condition associated with dysregulation of cellular  
XX phenotype. The method involves the administration of a composition  
XX containing a recombinant nucleic acid molecule (rNA) encoding a cyclic-  
XX AMP responsive element binding (CREB) protein having CREB biological  
XX activity to a patient, such that the CREB protein is expressed in  
XX target cells, and is sufficient to modulate the phenotype of the  
XX target cells. This method is useful for modulating the phenotype of  
XX target cell population, such as adipocytes, vascular smooth muscle cells,  
XX cardiomyocytes, hepatocytes, skeletal muscle, beta cells, pituitary,  
XX spermatocytes, oocytes, testicular fibroblasts, endothelial, neural  
XX cells (dopaminergic neural transplant cells), hippocampal neurons, cells  
XX of cortex and basal ganglia in a patient having or risk of developing  
XX obesity, diabetes, cardiovascular disease (congestive heart failure,  
XX cardiomyopathy), neurovascular disease (atherosclerosis, angina, acute  
XX myocardial infarction, stroke), pulmonary hypertension and amputation  
XX from peripheral vascular disease), post angioplasty restenosis,  
XX osteoarthritis, heart failure, and neurodegenerative diseases  
XX (Alzheimer's disease, Parkinson's disease, spinal transection, acute  
XX neuronal ischemia and depression). This method is also used to  
XX inhibit tumour neovascularisation.  
XX  
XX Sequence 327 AA;

Query Match 83.88% Score 93; DB 22; Length 327;  
Best Local Similarity 100.00% Pred. No. 1,96.06;  
Matches 19; Conservative 0; Mismatches 0; Gaps 0;  
QY 4 ELLSRKPSYRKLLNDLSSD 22  
DE 112 ELLSRKPSYRKLLNDLSSD 130  
XXXXXXXXXXXXXXXXXXXX  
RESULT 5  
AAB73291  
ID AAB73291 standard; Protein: 327 AA;  
XX  
AC AAB73291  
XX 29-MAY 2001 (first entry)  
DE CREB protein  
XX CREB; transgenic mouse; transcription factor; congestive heart failure;  
KW CHF.  
XX Unidentified.  
XX OS  
XX PN US6194632 B1.  
XX 27 FEB 2001.  
XX 18 DEC 1998; 98US (215098  
XX 18 DEC 1997; 97US 0068011  
XX (LEINZ) LEIDEN J M.  
XX Leiden JM;  
XX WPI: 2001 255289/26.  
XX Transgenic mice expressing CREB, useful as genetic models for  
XX congestive heart failure, e.g. progressive biventricular failure,  
XX cardiac dilation, decreased myocardial contractility, peripheral edema  
XX or intracardiac thrombi  
XX Dislosure: Fig 5; 19pp; English.  
XX The present invention relates to transgenic mice comprising a transgene  
XX under operational control of a myocyte specific promoter. The transgene  
XX encodes a protein having wild type CREB activity or dominant negative  
XX CREB activity. CREB (the present sequence) is a 43 kb basic leucine  
XX zipper transcription factor. The expression of the transgene leads to  
XX models of dilated cardiomyopathy or phenotypes associated as genetic  
XX transgenic mice are also useful for providing important basic information  
XX concerning the role of the CREB transcriptional pathway in regulation  
XX of cardiac myocyte function. These animals will also facilitate studies  
XX designed to identify new drugs that can decrease the morbidity and  
XX mortality associated with the disease.  
XX Sequence 327 AA;  
SQ

Query Match 83.88% Score 93; DB 22; Length 327;  
Best Local Similarity 100.00% Pred. No. 1,96.06;  
Matches 19; Conservative 0; Mismatches 0; Gaps 0;  
QY 4 ELLSRKPSYRKLLNDLSSD 22  
DE 112 ELLSRKPSYRKLLNDLSSD 130  
XXXXXXXXXXXXXXXXXXXX  
RESULT 6  
AAE00655  
ID AAE00655 standard; Protein: 328 AA;





XX Disclosure: Page 16; 34pp; English.

PS The present invention relates to a biomolecular substrate,

XX comprising a core molecular backbone, a fluorescent dye and a

CC second dye. The dye changes state if the biomolecular substrate

CC is covalently modified. The invention is useful for assaying

CC covalent biomolecular modification in a sample. For example, it

XX is useful for assaying protein kinase activity.

SV Sequence 24 AA;

Query Match 68 5%; Score 76; DP 22; Length 24;

Best Local Similarity 93.8%; Pred. No. 5.2e-05;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNDL 19

DE 7 EILSRPSPSYRKILNDL 22

AA065586

AA065586 standard; peptide: 22 AA.

XX

AC AA065586;

XX

DE 07-JAN-2002 (first entry)

XX

DE Mouse CREM protein KID domain fragment.

DE CREM, cAMP response element binding protein, nuclear, cytosolic,

XX cellular signaling; KID domain; CREM

XX

OS Mus sp.

XX

PN W0200171352 A2.

XX

PD 27-SEP-2001.

XX

XX

PF 19-MAR-2001; 2001WO-US08946.

XX

XX

PR 17-MAR-2000; 2000US-190705P.

XX

PA (SALK ) SALK INST BIOLOGICAL STUDIES.

XX

PI Mounting M, Warner B;

XX

DR WPI; 2001-607512/69

XX

XX

PI Composition for modulating intracellular complex formation, for

PI treating disorders associated with complex formation/disruption, is

PI specific for endogenous cellular protein or

PI protein-polynucleotide complexes -

XX

PS Enq; 16.5; P1 1; 28p; English.

XX

XX

XX The invention relates to compositions (I) specific for complexes or at

XX least one individual component of a complex. (I) is useful for mediating

XX complex formation. It is useful for modulating the interaction and/or

XX activity of intracellular complexes, especially nuclear protein

XX complexes, for the treatment of disorders associated with complex

XX formation/disruption e.g. cancer and disorder associated with metabolism

XX and cellular signaling. (I) is also useful for screening for complex

XX forming agents, for the treatment of disorders associated with complex

XX formation/disruption. The composition

XX includes endogenous cellular components which interact with the complex

XX or components in vivo and provide new targets for pharmaceutical and

XX therapeutic interventions, as well as recombinant, synthetic and

XX or other compounds which have complex or complex binding capacity, and

XX therefore may be candidates for pharmaceutical agents, cell lysates or

XX tissue homogenates may be screened for proteins or other compounds which

XX specifically bind to either the complex or the components. (I) can also

CC be employed to distinguish epitopes specific to the complex. The present

CC sequence represents the alpha A and alpha B regions in the KID domain of

CC mouse CREM protein.

XX

SV Sequence 22 AA;

Query Match 67.6%; Score 75; DP 22; Length 22;

Best Local Similarity 93.8%; Pred. No. 6.8e-05;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNDL 19

DE 7 EILSRPSPSYRKILNDL 22

AA00656

AA00656 standard; Protein; 271 AA.

XX

AC AA00656;

XX

PD 02 JUL 2001 (first entry)

XX

DE Human activating transcription factor-1 (ATF-1) protein.

XX

KW Human; cyclic adenosine mono phosphate; cell phenotype modulator; CREB;

KW cAMP responsive element binding protein; antidiabetic; cytosolic;

KW neuroprotective; neurotrophic; osteopathic; antiarthritis; antianginal;

KW antiatherosclerotic; vasotropic; cerebroprotective; antidepressant;

KW cardiac; hypotensive; obesity; cardiovascular disease; cardiomyopathy;

KW congestive heart failure; macrovascular disease; pulmonary hypertension;

KW acute myocardial infarction; stroke; peripheral vascular disease;

KW post angioplasty restenosis; heart failure; neurodegenerative disease;

KW Alzheimer's disease; Parkinson's disease; spinal transection;

KW acute neuronal ischaemia; tumour neovascularisation; ATF-1;

KW activating transcription factor-1.

XX

OS Homo sapiens.

XX

PN W0200129062 A2.

XX

PD 26-APR-2001.

XX

XX

PF 12-OCT-2000; 2000WO-US28316.

XX

PR 18-OCT-1999; 99US-0420060.

XX

XX

PA (UYTE ) UNIV TECHNOLOGY CORP.

PA (NAT ) NAT DEPT MEDICAL & RES CENT.

PA (USGO ) US DEPT VETERANS AFFAIRS.

XX

PI Reusch JE, Klemm DJ;

XX

DR WPI; 2001-290991/30.

XX

DR N PSDB; AAD003962.

XX

XX

PI Modulating cell phenotype in a patient having or risk of developing a

PI disease/condition linked with dysregulation of cellular phenotype,

PI comprises administering nucleic acid encoding cyclic AMP responsive

PI element binding protein -

XX

PS Claim 5, Page 154 155; 156pp; English.

XX

XX The patent discloses a method for modulating the phenotype of a target

XX cell population in a patient who has or is at risk of developing a

XX disease or condition associated with dysregulation of cellular

XX phenotype. The method involves the administration of a composition

XX containing a recombinant nucleic acid molecule (rNA) encoding a cyclic-

XX AMP responsive element binding (CREB) protein having CREB biological

XX activity to a patient, such that the CREB protein is expressed in

XX target cells, and is sufficient to modulate the phenotype of the

XX target cells. CREB protein is a transcription factor necessary and

XX sufficient to induce a modulation in cell phenotype and to induce cell





10 AAR70223 standard; peptide; 12 AA.  
XX  
AC AAR70223;  
XX  
DI 03-MAY-2001 (first entry)  
XX  
DE Synthetic KID sequence peptide.  
XX  
KW Riemann-Lee type, synthetic modification, protein kinase  
XX  
AS Synthetic.  
XX  
PN W020010748 A2.  
XX  
PD 01-FEB-2001.  
XX  
XX 27-JUL-2000; 2000W; 9840495.  
XX  
XX 27-JUL-1999; 9900-0145755.  
XX  
XX (GIAH) ONLY WITH KISS F-ONE.  
XX  
XX Riemann-Lee type.  
XX  
XX WPI: 2001-159725/16  
XX  
XX Novel double labeled biomolecular substrate, comprising core molecular  
XX back bone, 3,3'-di-4,4'-biphenyl, 4,4'-biphenyl, 4,4'-biphenyl, 4,4'-  
XX is useful for assaying covalent structural modifications of  
XX biomolecules.  
XX  
XX Disclosure: Page 16; 34pp; English.  
XX  
XX The present invention relates to a biomolecular substrate,  
XX comprising a core molecular backbone, a fluorescent dye and a  
XX second dye. The dye changes state if the biomolecular substrate  
XX is covalently modified. The invention is useful for assaying  
XX covalent biomolecular modification in a sample. For example, it  
XX is useful for assaying protein kinase activity.  
XX  
SQ Sequence 12 AA:  
  
Query Match 53.2%; Score 59; DP 22; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.012;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 KRPSYRKILNDL 19  
111111111111  
DB 1 KRPSYRKILNDL 12  
  
RESULT 15  
AAG65585  
DI AAG65585 standard; peptide; 22 AA.  
XX  
AA AAG65585;  
XX  
DI 07-JAN-2002 (first entry)  
XX  
XX C. elegans CREB protein KID domain fragment.  
XX  
XX CREB; intracellular complex; nuclear protein; cancer; cytostatic;  
XX cellular signaling; KID domain.  
XX  
XX Caenorhabditis elegans.  
XX  
XX W020010748 A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 19 MAR-2001; 2001W0-US08946.  
XX  
XX 17-MAR-2000; 2000US-190705P.  
XX  
PR

XX  
PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX  
PI Montminy M, Waegner B;  
XX  
DR WPI: 2001-607542/69.  
XX  
PT composition for modulating intracellular complex formation, for  
PT treating disorders associated with complex formation, disruption, is  
PT specific for endogenous cellular protein-protein or  
PT protein-polynucleotide complexes -  
XX  
XX Examples; Fig 1; 28pp; English.  
XX  
XX The invention relates to compositions (1) specific for complexes or at  
XX least one individual component of a complex. (1) is useful for modulating  
XX complex formation. It is useful for modulating the interaction and/or  
XX activity of intracellular complexes, especially nuclear protein-protein  
XX complexes, for the treatment of disorders associated with complex  
XX formation/disruption e.g. cancer and disorder associated with metabolism  
XX and cellular signaling. (1) is also useful for screening for complex  
XX formation/disruption and/or activity and for diagnosis of disorders  
XX associated with irregular complex formation/disruption. The composition  
XX includes endogenous cellular components which interact with the complexes  
XX or components in vivo and provide new targets for pharmaceutical and  
XX therapeutic interventions, as well as recombinant, synthetic and  
XX exogenous compounds which have complex or component binding capacity and  
XX that are useful for pharmaceutical agents. Cell lyzates or  
XX tissue homogenates may be screened for proteins or other compounds which  
XX specifically bind to either the complex or the components. (1) can also  
XX be employed to distinguish epitopes specific to the complex. The present  
XX sequence represents the alpha A and alpha B regions in the KID domain of  
XX C. elegans CREB protein.  
XX  
SQ Sequence 22 AA:  
  
Query Match 51.4%; Score 57; DP 22; Length 22;  
Best Local Similarity 75.0%; Pred. No. 0.047;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 4 ELLSRKPSYRKILNDL 19  
111111111111  
DB 7 EQLNRKPSYRMILKDL 22  
  
Search completed: January 2, 2003, 12:28:04  
Job time : 32 secs



GenPro version 5.1.3  
Copyright (c) 1993-2003 Compugen Ltd.

M protein protein search, using sw model

Run on: January 2, 2003, 12:26:41 ; Search time: 31 seconds  
(without alignment)  
98,863 Million eval updates/sec

11'000 OS 09 786 317 2

Portlet score: 109

Sequence: 118LPPASLGI6HAYHATGRSS1 23

Scoring table: Blast062

Gap: 10.0 ; Gapext: 0.5

Searched: 908470 seqs, 136256620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum hit seq length: 5

Maximum hit seq length: 200000000

Post processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database: A Geneset to 1002\*

1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
2	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
3	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
4	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
5	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
6	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
7	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
8	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
9	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
10	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
11	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
12	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
13	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
14	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
15	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
16	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
17	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
18	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
19	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
20	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
21	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
22	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1
23	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1	118LPPASLGI6HAYHATGRSS1

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Prod. No.	Score	Match	Length	DB	Hit	Description
1	109	100.0	23	AA081936	1	Receptor phosphorylation
2	76	69.7	26	AA073293	1	Calmodulin-binding
3	66	60.6	21	AA083068	1	M13 segment of Smo
4	66	60.6	416	AA083069	1	Calcium sensor G85
5	65	59.6	20	AA071650	1	Swath angle-type
6	65	59.6	20	AA050818	1	Turkey protein cal
7	63	57.8	18	AA017119	1	Calmodulin antagou
8	63	57.8	18	AA073197	1	Calmodulin antagou
9	60	55.0	21	AA083070	1	Partial amino acid
10	58	53.2	1953	AA084351	1	Protein MYLK d110

ALLISUMMARIES

RESULT 1

AA081936

118LPPASLGI6HAYHATGRSS1 23 AA

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CC  
CC  
CC  
CC  
CC  
CC  
CC  
SQ

Disclosure: Page 38; 45pp; Japanese.

This sequence represents a heptide phosphorylation region.  
The invention relates to a monitor protein (I) for measuring  
phosphorylation of a protein. (I) comprises a protein containing a  
phosphorylation region and a characteristically variable region, where  
characteristics vary due to a change in the stereostructure. It is  
conveniently applicable for use in *in vivo* determination without needing  
radioisotopes. (I) is useful for the measurement of phosphorylation of  
protein, and for *in vivo* determination without needing radioisotopes  
e.g. in studying phosphorylation reaction and screening kinases and  
promoters and inhibitors of phosphorylation

Sequence 23 AA;

Sequence 23 AA:

Query Match:	100.0%	Score 109,	DB 21;	Length 23;
Best local Similarity	100.0%	Pred. No. 3.5e-10;		
Matches 23; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 TSLRRASLGTCHAVRAIGRLSST 23  
|||||  
Db 1 TSLRRASLGTCHAVRAIGRLSST 23

RESULT 4  
AAW74294  
ID AAW74294 standard, peptide, 20 AA.

AC AAW73293;

08-FRB-1999 (first entry)

Calmodulin-binding peptide

KW Calmodulin-binding peptide; ligand detection; green fluorescent protein;  
 YW ligand-dependent fluorescent resonant energy transfer; FEET.

[illegible]

PH 100-18378 A1.

6901 - 1.000 - 6C

111

23-APR-1998: 58WC-11508109

XX 24 APR 1947  
PR 9713-0040000

PAUL J. HAYES, UNIVERSITY OF ROCHESTER

Bi Persichini A.

XX  
ADP - 1468-583831 AG

AA	New complex of two green fluorescent proteins connected by
PI	ligand-binding peptide useful for, e.g. measuring levels of
PI	specific ligands in cells, monitoring changes, and for identifying
PI	agents with ligand binding activity

PS Claim 4: Page 25: English

This sequence represents a calmodulin-binding peptide, and is used as a primary ligand binding peptide in the method of the invention. The method is for monitoring the amount of a primary ligand (1) in a cell by forming a green fluorescent protein (GFP) complex (A) consisting of: (i) a first GFP; (ii) a (1)-binding peptide attached to the first GFP at its N-terminus; and (iii) a second GFP attached to the C-terminus of the (1)-binding peptide, where the first GFP is excited at wavelength W1 and emits fluorescence at wavelength W2, while the second GFP is excited at W2 and emits at wavelength W3. The complex is introduced into a cell, and the base amount of fluorescence emission at W3 when the cell is excited at W1 is measured. The fluorescence emission over time recorded at W3, when excited at W1 is also measured, and is then compared with the base

emission. Any change in emission indicates a change in the amount of (1). The method is used to determine maximal and resting levels of (1) in different cell types and at different stages of the cell cycle, also spatio-temporal changes in (1)-binding activity during cellular events. It may be modified to determine the amount of a secondary ligand in a cell. The method is based on ligand dependent fluorescent resonant energy transfer (FRET) between the two GFP.

sequence 26 AA;

Query Match 69.7%; Score 76; BP 19; Length 26;  
Best local Similarity 78.3%; Pred. NO. 5.6e-05;  
Matches 19; Conservative 0; Mismatches 5; Indels

```

07      1 TSLRRASLCTCHAVRAICRISST 23
      || || || || || || || || || ||
08      2 TSSDPEKKNLTCHAVRAICRISST 24

```

## 3. RESULTS

ABR83068	
ID	ABR83068 standard; Peptide; 21 AA.
XX	
AC	ABR83068;

06-SEP-2002 (first entry)

DE M23 segment of smooth muscle myosin light chain kinase.

KW Biosensor protein; green fluorescent protein; GFP; calmodulin sensor;  
KW fluorescence; smooth muscle; myosin light chain kinase.

OS Synthetic.

PN EPI209167-A1.

29-MAY-2009

21-NOV-2001: 2001EF-0127775

22	May	2000	2000.F-0356047
23	May	2000	2000.F-0356048
24	May	2000	2000.F-0356049
25	May	2000	2000.F-0356050
26	May	2000	2000.F-0356051
27	May	2000	2000.F-0356052
28	May	2000	2000.F-0356053
29	May	2000	2000.F-0356054
30	May	2000	2000.F-0356055
31	May	2000	2000.F-0356056
32	May	2000	2000.F-0356057
33	May	2000	2000.F-0356058
34	May	2000	2000.F-0356059
35	May	2000	2000.F-0356060
36	May	2000	2000.F-0356061
37	May	2000	2000.F-0356062
38	May	2000	2000.F-0356063
39	May	2000	2000.F-0356064
40	May	2000	2000.F-0356065
41	May	2000	2000.F-0356066
42	May	2000	2000.F-0356067
43	May	2000	2000.F-0356068
44	May	2000	2000.F-0356069
45	May	2000	2000.F-0356070
46	May	2000	2000.F-0356071
47	May	2000	2000.F-0356072
48	May	2000	2000.F-0356073
49	May	2000	2000.F-0356074
50	May	2000	2000.F-0356075
51	May	2000	2000.F-0356076
52	May	2000	2000.F-0356077
53	May	2000	2000.F-0356078
54	May	2000	2000.F-0356079
55	May	2000	2000.F-0356080
56	May	2000	2000.F-0356081
57	May	2000	2000.F-0356082
58	May	2000	2000.F-0356083
59	May	2000	2000.F-0356084
60	May	2000	2000.F-0356085
61	May	2000	2000.F-0356086
62	May	2000	2000.F-0356087
63	May	2000	2000.F-0356088
64	May	2000	2000.F-0356089
65	May	2000	2000.F-0356090
66	May	2000	2000.F-0356091
67	May	2000	2000.F-0356092
68	May	2000	2000.F-0356093
69	May	2000	2000.F-0356094
70	May	2000	2000.F-0356095
71	May	2000	2000.F-0356096
72	May	2000	2000.F-0356097
73	May	2000	2000.F-0356098
74	May	2000	2000.F-0356099
75	May	2000	2000.F-0356100
76	May	2000	2000.F-0356101
77	May	2000	2000.F-0356102
78	May	2000	2000.F-0356103
79	May	2000	2000.F-0356104
80	May	2000	2000.F-0356105
81	May	2000	2000.F-0356106
82	May	2000	2000.F-0356107
83	May	2000	2000.F-0356108
84	May	2000	2000.F-0356109
85	May	2000	2000.F-0356110
86	May	2000	2000.F-0356111
87	May	2000	2000.F-0356112
88	May	2000	2000.F-0356113
89	May	2000	2000.F-0356114
90	May	2000	2000.F-0356115
91	May	2000	2000.F-0356116
92	May	2000	2000.F-0356117
93	May	2000	2000.F-0356118
94	May	2000	2000.F-0356119
95	May	2000	2000.F-0356120
96	May	2000	2000.F-0356121
97	May	2000	2000.F-0356122
98	May	2000	2000.F-0356123
99	May	2000	2000.F-0356124
100	May	2000	2000.F-0356125

PA (CKAS) DEAPAKI NAT RES (NSI)

DT Nakai T.

THE UNIVERSITY OF CHICAGO

UK N-151B; APB 8,900.

PT producing a biosensor protein capable of regulating fluorescence

PT property of green fluoresce protein comprises predicting an amino acid

PT residue that affects fluorescence, and fusing with a functional

PT molecule -

xx	Example 1	Page 20	Page 499	Example 2
xx				

The invention relates to producing a biosensor protein capable of regulating a fluorescence property of green fluorescent protein (GFP). This comprises predicting an amino acid affecting a fluorescence property of GFP, producing fusion proteins with GFP and functional molecule(s), reacting with a factor affecting the conformation of the functional molecules and screening a fusion protein exhibiting a change in the fluorescence property. The method is useful for producing a biosensor protein (especially a calmodulin-sensing biosensor protein) capable of regulating a fluorescence property of GFP. The method of producing proteins with a unique structure produces proteins with a high sensitivity, unlike prior art methods producing proteins with low sensitivity. A specific detection device is not needed. The current sequence represents M2 segment of smooth muscle myosin light chain kinase amino acid sequence. This is used in the context of the invention as a functional molecule.

Sequence	2L AA;
SO	





08 NOV 2001.  
 02 MAY 2001. 2001W00314 Cite.  
 03 MAY 2000. 2000J05 0563286.  
 (AMGEN ) AMGEN INC.  
 Priya D., Liu C., Chrestham JC., Boone F., Gudas JM.  
 WPI: 2002-464878/50.  
 Novel vehicle peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.  
 Claim 39; Page 53; 17pp; English.  
 The present invention describes a vehicle-peptide molecule (1) or its multimers. (1) can have anti-inflammatory, anti-tumor, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological, anti-tumour, anorectic, anti-fertility, haemostatic, dermatological and neuroprotective activities. (1) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (1) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their proteins of interest in a biological sample. Additionally, (1) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, infertility, and neurological degenerative diseases. (1), comprising EPO mimetic compounds are useful for treating disorders characterised by low red blood cell levels such as anemia. The EPO-mimetic comprising compounds are useful for treating conditions that involve an existing megalarycytoblastic deficiency or an expected megalarycytoblastic deficiency, such as thrombocytopaenia, aplastic anemia, metastatic tumour which result in thrombocytopaenia, systemic lupus erythematosus, and Fanconi's syndrome. AB672463 to AB674426 and AB636695 to AB637777 represent amino acid and nucleic acid sequences used in the exemplification of the present invention.  
 Sequence 18 AA;  
 Query Match 67.8%; Score 63; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 0.0041;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 27 10 TGHAVRAICGLSS 22  
 11 1111111111111111  
 16 6 TGHAVRAICGLSS 18  
 06 SEP 2002 (first entry)  
 AB663076 standard; Peptide; 21 AA.  
 AB663076;  
 06 SEP 2002 (first entry)  
 Partial amino acid sequence of myosin light chain kinase protein.  
 Biosensor protein; green fluorescent protein; GFP; calmodulin sensor;  
 Fluorescence; myosin light chain kinase.  
 Gradient titred.  
 EP1209167 A1.  
 29 MAY 2002.  
 21 NOV 2001; 2001EP 0127775.  
 22 NOV-2000; 2000JP 0356047.  
 (AKAZ ) AKAZAKI NAH KIDA INST.  
 Nakai J.  
 WPI: 2002-464878/50.  
 Producing a biosensor protein capable of regulating fluorescence property of green fluorescent protein comprises predicting an amino acid residue that affects fluorescence, and fusing with a functional molecule.  
 Claim 14(b); Page 39; 4pp; English.  
 The invention relates to producing a biosensor protein capable of regulating a fluorescence property of green fluorescent protein (GFP). This comprises predicting an amino acid affecting a fluorescence property of GFP, producing fusion proteins with GFP and functional molecule(s), reacting with a factor affecting the conformation of the functional molecules and screening a fusion protein exhibiting a change in the fluorescence property. The method is useful for producing a biosensor protein (especially a calmodulin-sensing biosensor protein) capable of regulating a fluorescence property of GFP. The method of producing proteins with a unique structure produces proteins with a high sensitivity, unlike prior art methods producing proteins with low sensitivity. A specific detection device is not needed. The current sequence represents a partial amino acid sequence of myosin light chain kinase protein that is used in the construction of a biosensor of the invention.  
 Sequence 21 AA;  
 Query Match 55.0%; Score 60; DB 23; Length 21;  
 Best Local Similarity 71.4%; Pred. No. 0.014;  
 Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 27 2 SRRASLGTCGHAVRAICGLSS 22  
 11 1111111111111111  
 16 1 CSRRKYNEYCHAVRAICGLSS 21  
 RESULT 10  
 AA084351  
 10 AA084351 standard; Protein; 1953 AA.  
 XX AA084351;  
 08 MAY-2002 (first entry)  
 Protein MYLK differentially expressed in breast cancer tissue.  
 Human; diagnosis of breast cancer; endometrial cancer; breast tumour;  
 MAF; mitotic activity index; cytostatic  
 Homo sapiens.  
 W0200210436 A2.  
 07-FEB 2002.  
 27-JUL-2001; 2001W00324642.  
 28-JUL 2000; 2000J05 222094P.  
 (BGLIM ) BRIGHAM & WOMENS HOSPITAL INC.  
 (BAAK/) BAAK J.  
 Baak J., Mutter GL;  
 WPI: 2002-180084/23.  
 N PSDH; ABK45571.  
 22 NOV-2000; 2000JP 0356047.  
 (AKAZ ) AKAZAKI NAH KIDA INST.  
 Nakai J.  
 WPI: 2002-464878/50.  
 Producing a biosensor protein capable of regulating fluorescence property of green fluorescent protein comprises predicting an amino acid residue that affects fluorescence, and fusing with a functional molecule.  
 Claim 14(b); Page 39; 4pp; English.  
 The invention relates to producing a biosensor protein capable of regulating a fluorescence property of green fluorescent protein (GFP). This comprises predicting an amino acid affecting a fluorescence property of GFP, producing fusion proteins with GFP and functional molecule(s), reacting with a factor affecting the conformation of the functional molecules and screening a fusion protein exhibiting a change in the fluorescence property. The method is useful for producing a biosensor protein (especially a calmodulin-sensing biosensor protein) capable of regulating a fluorescence property of GFP. The method of producing proteins with a unique structure produces proteins with a high sensitivity, unlike prior art methods producing proteins with low sensitivity. A specific detection device is not needed. The current sequence represents a partial amino acid sequence of myosin light chain kinase protein that is used in the construction of a biosensor of the invention.  
 Sequence 21 AA;  
 Query Match 55.0%; Score 60; DB 23; Length 21;  
 Best Local Similarity 71.4%; Pred. No. 0.014;  
 Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 27 2 SRRASLGTCGHAVRAICGLSS 22  
 11 1111111111111111  
 16 1 CSRRKYNEYCHAVRAICGLSS 21













RESULT 2  
US-08-542-927-6  
; Sequence 6, Application US/08542927  
; Patent No. 5998580  
; GENERAL INFORMATION:  
; APPLICANT: Fay, Fredric  
; APPLICANT: Carraway, Robert  
; APPLICANT: Ikebe, Mitsuo  
; APPLICANT: Walker, Jeffrey  
; TITLE OF INVENTION: PHOTSENSITIVE CAGED MACROMOLECULES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/542,927  
; FILING DATE: 13-OCT-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, F. J.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/AGENT NUMBER: 04020/055901  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-5000  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: both  
; MOLECULE TYPE: protein  
; FEATURE:  
; OTHER INFORMATION: Xaa at position 5 contains a caged tyrosine.  
US-08-542-927-6  
Query Match 62.4%; Score 68; DB 2; Length 20;  
Best Local Similarity 78.9%; Pred. No. 9.8e-05;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4 PRASLSTGHAVRAIGRLSS 22  
DB 2 PRKWKQTCGHAVRAIGRLSS 20  
RESULT 3  
5182262-10  
; Patent No. 5182262  
; APPLICANT: LEIO, THOMAS  
; TITLE OF INVENTION: CALMODULIN BINDING PEPTIDE DERIVATIVES  
; OF NON ERYTHROID ALPHA SPECTRIN  
; NUMBER OF SEQUENCES: 15  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/218,172  
; FILING DATE: 02-MAR-1989  
; SEQ ID NO: 10:  
; LENGTH: 22  
5182262-10  
Query Match 60.6%; Score 66; DB 6; Length 22;  
Best Local Similarity 75.0%; Pred. No. 0.00023;  
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 PRASLSTGHAVRAIGRLSS 22  
DB 3 PRKWKQTCGHAVRAIGRLSS 22  
RESULT 4  
US-08-818-253-10  
; Sequence 10, Application US/08818253  
; Patent No. 5999204  
; GENERAL INFORMATION:  
; APPLICANT: Tsien, Roger Y.  
; APPLICANT: Miyawaki, Atsushi  
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
; DETECTION OF ANALYTES  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/019,253  
; FILING DATE: 14-MAR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Ph.D., Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/AGENT NUMBER: 07257/043001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-818-253-10  
Query Match 59.6%; Score 65; DB 2; Length 20;  
Best Local Similarity 78.9%; Pred. No. 0.0003;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4 PRASLSTGHAVRAIGRLSS 22  
DB 2 PRKWKQTCGHAVRAIGRLSS 20  
RESULT 5  
US-08-542-927-5  
; Sequence 5, Application US/08542927  
; Patent No. 5998580  
; GENERAL INFORMATION:  
; APPLICANT: Fay, Fredric  
; APPLICANT: Carraway, Robert  
; APPLICANT: Ikebe, Mitsuo  
; APPLICANT: Walker, Jeffrey  
; TITLE OF INVENTION: PHOTSENSITIVE CAGED MACROMOLECULES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA

COUNTRY: USA  
ZIP: 14604  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Patent In Release #1.0, Version #1.40  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/09/942,927  
FILING DATE: 13 OCT 1995  
CLASSIFICATION: 540  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul L.  
REGISTRATION NUMBER: 30,162  
REFERENCE/AGENT NUMBER: 04629/056001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5029  
TELEFAX: 617/542-8996  
TELEX: 260154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US 08 542 927 5

Query Match 59.6% Score 65; DB 2; Length 20;  
Best Local Similarity 78.9% Pred. No. 0.0004;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

27 4 KRASLTGIGHAVRAIGRLSS 22  
II IIIIIIIIIII

DB 2 RPKWKIKGHAVRAIGRLSS 20

## RESULT 4

US 08 542 927 10  
Sequence 10, Application US/08018252B  
Patent No. 6197928  
GENERAL INFORMATION:  
APPLICANT: Tsien, Roger Y.  
APPLICANT: MIYAWAKI, ATSUSHI  
TITLE OF INVENTION: IMPROVED PROTEIN SENSORS FOR  
TITLE OF INVENTION: DETECTOR OF ANALYTES  
FILE REFERENCE: 07257/042001  
CURRENT APPLICATION NUMBER: 08/09/942,928  
CURRENT FILING DATE: 1997 04 14  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 10  
LENGTH: 20  
TYPE: PRO  
ORGANISM: Melospiza gallopavo  
US 08 542 927 10

Query Match 59.6% Score 65; DB 4; Length 20;  
Best Local Similarity 78.9% Pred. No. 0.0004;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

27 4 KRASLTGIGHAVRAIGRLSS 22  
II IIIIIIIIIII

DB 2 RPKWKIKGHAVRAIGRLSS 20

## RESULT 7

US 08 542 927 4  
Sequence 4, Application US/080437927  
Patent No. 6366257  
GENERAL INFORMATION:  
APPLICANT: Persechini, Anthony  
TITLE OF INVENTION: DETECTION BY FREE CHANGES OF LIGAND

Query Match 59.6% Score 65; DB 4; Length 20;  
Best Local Similarity 78.9% Pred. No. 0.0004;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

TITLE OF INVENTION: BINDING BY GTP-BINDING PROTEINS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14604  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Patent In Release #1.0, Version #1.40  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/08/842,822  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: BRAMAN, SUSAN J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/AGENT NUMBER: 176760170  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US 08 842 822 4

Query Match 59.6% Score 65; DB 4; Length 20;  
Best Local Similarity 78.9% Pred. No. 0.0004;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 KRASLTGIGHAVRAIGRLSS 22  
II IIIIIIIIIII

DB 2 RPKWKIKGHAVRAIGRLSS 20

## RESULT 8

US 09 316 919 26  
Sequence 26, Application US/09316919  
Patent No. 6469154  
GENERAL INFORMATION:  
APPLICANT: Tsien, Roger Y.  
APPLICANT: Baird, Geoffrey  
TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS  
FILE REFERENCE: 07257/070091  
CURRENT APPLICATION NUMBER: 09/09/316,919  
CURRENT FILING DATE: 1999 05 21  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 26  
LENGTH: 20  
TYPE: PRO  
ORGANISM: Melospiza gallopavo  
US 09 316 919 26

Query Match 59.6% Score 65; DB 4; Length 20;  
Best Local Similarity 78.9% Pred. No. 0.0004;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 KRASLTGIGHAVRAIGRLSS 22  
II IIIIIIIIIII

DB 2 RPKWKIKGHAVRAIGRLSS 20

## RESULT 9

US 08 542 927 7



APPLICANT: Schottkemaker, Johanna  
TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCYTIO  
TITLE OF INVENTION: INFLUENZA AND NON SYNCYTIUM INDUCING VARIANTS OF THE HUMAN IMMUN  
FILE REFERENCE: 9259,25  
CURRENT APPLICATION NUMBER: 03/08/722,015A  
CURRENT FILING DATE: 1996 11 19  
NUMBER OF SEQ ID NOS: 258  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 149  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Human immunodeficiency Virus Isolate H72.S  
US 08 722 015A 149

Query Match 43.1% Score 47 Db 4 Length 35  
Best Local Similarity 52.9% Pred. No. 0.44  
Matches 9 Conservative 4 Mismatches 5 Indels 0 Gaps 0

27 4 KRASIGTGHAVRAIGRL 26  
11 111111111111  
14 10 KRISGPGRAFTIGQI 26

RESULT 14  
US 08 722 015A 148  
Sequence 148, Application US/08/22015A  
Patent No. 637988

GENERAL INFORMATION:  
APPLICANT: Schottkemaker, Johanna  
APPLICANT: Schottkemaker, Johanna  
TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCYTIO  
TITLE OF INVENTION: INFLUENZA AND NON SYNCYTIUM INDUCING VARIANTS OF THE HUMAN IMMUN  
FILE REFERENCE: 9259,25  
CURRENT APPLICATION NUMBER: US/08/722,015A  
CURRENT FILING DATE: 1996 11 19  
NUMBER OF SEQ ID NOS: 258  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 148  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus Isolate H72.S  
US 08 722 015A 148

Query Match 40.4% Score 44 Db 4 Length 35  
Best Local Similarity 47.1% Pred. No. 1.3  
Matches 8 Conservative 4 Mismatches 5 Indels 0 Gaps 0

27 4 KRASIGTGHAVRAIGRL 26  
11 111111111111  
14 10 KRISGPGRAFTIGQI 26

RESULT 15  
US 08 722 015A 144  
Sequence 144, Application US/08/22015A  
Patent No. 637984

GENERAL INFORMATION:  
APPLICANT: Schottkemaker, Johanna  
APPLICANT: Schottkemaker, Johanna  
TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCYTIO  
TITLE OF INVENTION: INFLUENZA AND NON SYNCYTIUM INDUCING VARIANTS OF THE HUMAN IMMUN  
FILE REFERENCE: 9259,25  
CURRENT APPLICATION NUMBER: US/08/722,015A  
CURRENT FILING DATE: 1996 11 19  
NUMBER OF SEQ ID NOS: 258  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 144  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Human immunodeficiency Virus Isolate H72-25.S  
US 08 722 015A 144

Query Match 38.5% Score 42 Db 4 Length 35

Best Local Similarity 47.1% Pred. No. 2.8  
Matches 8 Conservative 4 Mismatches 5 Indels 0 Gaps 0  
QY 4 KRASIGTGHAVRAIGRL 26  
11 111111111111  
Db 10 KRISGPGRAFTIGQI 26  
Search completed: January 2, 2003, 12:29:47  
Job time : 14 secs







; TITLE OF INVENTION: Identification of Essential Genes in

(continued) THE ECONOMIC AND SOCIAL

US-09-815-242-11922

Query Match 49.44% Score 443 DB 107 Length 4773  
Best Local Similarity 47.88% Pred. No. 217  
Matches 111 Conservative 21 Mismatches 63 Indels 4 Gaps 11

27 1 ISLRASLGTGH AVRAVLR 19  
DB 70 LSLRSLGTGHLLVPTIKALAK 92

RESULT 6

US-09-867-550-344  
Sequence 334 Application US/09867550  
Patent No. US20020082206A1

GENERAL INFORMATION:

APPLICANT: Leach, Martin D.

APPLICANT: Moharabadi, Foad.

APPLICANT: Coley, Pamela

APPLICANT: Law, Debbie

APPLICANT: Topper, James

TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atharogenic Cells and

TITLE OF INVENTION: Therapy

FILE REFERENCE: 21492-913 (Out 4-13)

CURRENT APPLICATION NUMBER: 5575/867,550

PRIOR FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: US20020082206A1

PRIOR FILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 2125

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID No 344

LENGTH: 81

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

Location: (48)

OTHER INFORMATION: wherein Xaa may be any one of Ile or Met

US-09-867-550-344

Query Match 47.66% Score 417 DB 107 Length 817  
Best Local Similarity 46.78% Pred. No. 617  
Matches 107 Conservative 0 Mismatches 5 Indels 0 Gaps 0

27 1 ISLRASLGTGHAVR 19  
DB 29 ISLRASLGTGHAVR 43

RESULT 7

US-09-815-242-11922  
Sequence 10936 Application US/09815242  
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Baselbeck, Robert

APPLICANT: Ohlson, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert L.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITPA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 66/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2001-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2001-11-27  
PRIOR APPLICATION NUMBER: 60/257,941  
PRIOR FILING DATE: 2001-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID No 10937  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-815-242-10937

Query Match 47.66% Score 417 DB 107 Length 461  
Best Local Similarity 46.78% Pred. No. 443  
Matches 87 Conservative 2 Mismatches 5 Indels 0 Gaps 0

QY 2 SRRASLGTGHAV 14  
DB 74 AQAQSLGTGHAV 86

RESULT 8

US-09-815-242-12112  
Sequence 12112 Application US/09815242  
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Baselbeck, Robert

APPLICANT: Ohlson, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert L.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITPA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2001-10-23

FILE REFERENCE: ELITPA.011A

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,941

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID No 12112

LENGTH: 454

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-815-242-12112

Query Match 47.66% Score 417 DB 107 Length 454  
Best Local Similarity 46.78% Pred. No. 507  
Matches 111 Conservative 4 Mismatches 5 Indels 1 Gaps 1

QY 5 SRRASLGTGHAV KATGRSS 22  
DB 72 LQAQLGTGHAVQAALFELSA 92

RESULT 9  
US-09-738-626-4263  
Sequence 4263, Application US/09738626  
Publication No. US20020197605A1  
GENERAL INFORMATION:  
APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YUKOI, HARUHIKO  
APPLICANT: TATEISHI, NAKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: US 09-738-626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 00/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: Patent In ver. 3.0  
SEQ ID NO 4263  
LENGTH: 575  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-4263

Query Match 37.2% Score 40.5; DB 9; Length 575;  
Best Local Similarity 64.3%; Pred. No. 66;  
Matches 9; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
QY 11 GHA-VRAIGRLSST 23  
JL :|||||:  
DB 525 GHVHRAIGRVSGT 538

RESULT 10  
US-09-764-864-937  
Sequence 937, Application US/09764864  
Patent No. US20020132753A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PIZ23  
CURRENT APPLICATION NUMBER: US 09-764-864  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed (consult PALM or file wrapper)  
NUMBER OF SEQ ID NOS: 1792  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 937  
LENGTH: 212  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-764-864-937

Query Match 36.7% Score 40; DB 10; Length 212;  
Best Local Similarity 64.3%; Pred. No. 26;  
Matches 9; Conservative 1; Mismatches 4; Indels 4; Gaps 0;  
QY 8 LGTGHAVRAIGRLS 21  
JL :|||||:  
DB 132 LGAGVSVRAAGRAS 145

RESULT 11  
US-09-738-626-4486

Sequence 4486, Application US/09738626  
Publication No. US20020197605A1  
GENERAL INFORMATION:  
APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YUKOI, HARUHIKO  
APPLICANT: TATEISHI, NAKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: US 09-738-626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: Patent In ver. 3.0  
SEQ ID NO 4486  
LENGTH: 220  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-4486

Query Match 36.7% Score 40; DB 9; Length 220;  
Best Local Similarity 52.6%; Pred. No. 27;  
Matches 10; Conservative 3; Mismatches 4; Indels 2; Gaps 1;  
QY 7 SLATGHAVRAIG-RLSST 23  
JL :|||||:  
DB 140 ALGVDHAFRRIGLRITAT 158

RESULT 12  
US-09-737-149-25  
Sequence 25, Application US/09737149  
Patent No. US20020077466A1  
GENERAL INFORMATION:  
APPLICANT: Spaderna, Steven K  
APPLICANT: Quinn, Kerry E.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Muratidhara, Padiguru  
APPLICANT: Spytsek, Kimberly A.  
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
FILE REFERENCE: 15949-020 CIP  
CURRENT APPLICATION NUMBER: US 09-737-149  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/170,564  
PRIOR FILING DATE: 1999-12-14  
PRIOR APPLICATION NUMBER: 60/173,165  
PRIOR FILING DATE: 1999-12-27  
PRIOR APPLICATION NUMBER: 60/173,362  
PRIOR FILING DATE: 1999-12-27  
PRIOR APPLICATION NUMBER: 60/173,544  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 60/174,404  
PRIOR FILING DATE: 2000-01-04  
PRIOR APPLICATION NUMBER: 60/174,962  
PRIOR FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: 60/223,929  
PRIOR FILING DATE: 2000-08-09  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 25  
LENGTH: 3034  
TYPE: PRT



00 25 SLKRASLEU 34

Search completed: January 2, 2003, 12:36:12  
Job time : 8.5 secs



```

1  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURE
2  FILE OF INVENTION: METHODS OF USE THEREOF
3  FILE REFERENCE: 241,210
4  CURRENT APPLICATION NUMBER: US2009/0791,537
5  CURRENT FILING DATE: 2001-02-22
6  NUMBER OF SEQ ID NOS: 153055
7  SOFTWARE: PatentIn version 3.0
8  SEQ ID NO: 11298

```

PCT-US96-16603-6

RESULT 5  
US-09-989-025A-6  
, sequence 6, Application 09/0909025A





```

PCT-US96-16603-5
; Sequence 5, Application PC/TUS9616603
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL CENTER
; TITLE OF INVENTION: PHOTOSENSITIVE CAGED NUCLEOTIDES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/16603
; FILING DATE: 15-OCT-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/542,927
; FILING DATE: 13-OCT-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 42,983
; REFERENCE/EXCERPT NUMBER: 01020/055W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
PCT-US96-16603-5

Query Match 59.68; Score 65; DB 1; Length 20;
Best Local Similarity 78.98; Pred. No. 0.0052;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RRASLGTHAVRAIGRLSS 22
II | | | | | | | | | |
DB 2 RRKWKTHAVRAIGRLSS 20

RESULT 11
PCT-US98-08109-4
; Sequence 4, Application PC/TUS9808109
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; TITLE OF INVENTION: DETECTION BY FREEZING CHANGES OF LIGAND
; TITLE OF INVENTION: BINDING BY GTP FUSION PROTEINS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARPAVE, DEVANE & FOWLE LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: PCT/US98/08109
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/842,322
; FILING DATE: 24-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 20,727
; REFERENCE/EXCERPT NUMBER: 006/0171
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US98-08109-4

Query Match 59.68; Score 65; DB 1; Length 20;
Best Local Similarity 78.98; Pred. No. 0.0052;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 PRASLGTHAVRAIGRLSS 22
II | | | | | | | | | |
DB 2 RRKWKTHAVRAIGRLSS 20

RESULT 12
US-08-919-143-10
; Sequence 10, Application US/08919143
; GENERAL INFORMATION:
; APPLICANT: Tseu, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,143
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/818,252
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Baile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,447
; REFERENCE/EXCERPT NUMBER: 005/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-919-143-10

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Query Match 59.6%; Score 65; DB 13; Length 20;  
Best Local Similarity 78.9%; Pred. No. 0.0052;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

27 4 PRASADIGHAVARAIGRESS 22  
11 | | | | | | | | | |  
DB 2 RRKWKIGHAVARAIGRESS 20

RESULT 14  
US 09 416 920 26  
Sequence 26; Application US/09416920

GENERAL INFORMATION:  
APPLICANT: Isobe, Keiji Y.  
APPLICANT: Baird, Geoffrey  
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS  
FILE REFERENCE: 07252/042001  
CURRENT APPLICATION NUMBER: US/09416920  
CURRENT FILING DATE: 1999 05 21  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID No 26  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Meleagris gallopavo

US 09 416 920 26

Query Match 59.6%; Score 65; DB 17; Length 20;  
Best Local Similarity 78.9%; Pred. No. 0.0052;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

27 4 PRASADIGHAVARAIGRESS 22  
11 | | | | | | | | | |  
DB 2 RRKWKIGHAVARAIGRESS 20

RESULT 14  
US 09 416 920A 26  
Sequence 26; Application US/09416920A

GENERAL INFORMATION:  
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
APPLICANT: Isobe, Keiji Y.  
APPLICANT: Baird, Geoffrey  
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS  
FILE REFERENCE: PENDING  
CURRENT APPLICATION NUMBER: US/09416920A  
CURRENT FILING DATE: 1999 05 21  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID No 26  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Meleagris gallopavo

US 09 416 920A 26

Query Match 59.6%; Score 65; DB 17; Length 20;  
Best Local Similarity 78.9%; Pred. No. 0.0052;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

27 4 PRASADIGHAVARAIGRESS 22  
11 | | | | | | | | | |  
DB 2 RRKWKIGHAVARAIGRESS 20

RESULT 14  
US 09 416 920 10  
Sequence 10; Application US/09416920

GENERAL INFORMATION:  
APPLICANT: Isobe, Keiji Y.  
APPLICANT: Miyawaki, Atsushi  
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
TITLE OF INVENTION: DETECTION OF ANALYTES  
FILE REFERENCE: 07252/042001

CURRENT APPLICATION NUMBER: US/09416920  
CURRENT FILING DATE: 2000 04 20  
FILE 5 APPLICATION NUMBER: US/09416920  
PRIOR FILING DATE: 1997 04 14

NUMBER OF SEQ ID NOS: 66  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID No 10  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Meleagris gallopavo

US-09-554 000-10

Query Match 59.6%; Score 65; DB 19; Length 20;  
Best Local Similarity 78.9%; Pred. No. 0.0052;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

27 4 PRASADIGHAVARAIGRESS 22  
11 | | | | | | | | | |  
DB 2 RRKWKIGHAVARAIGRESS 20

Search completed: January 2, 2003, 12:55:22  
Job time: 137 secs



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CompuLink version 5.1.13

M protein protein search, using SW model

Run on: January 2 2003, 12:28:11 : Search time 11.5 seconds  
(without alignments)  
141.096 Million cell updates/sec

Index: US 09 786 317 2

Perfect score: 100

Sequence: 1 ISLERASLTGTHAVRAVRLSST 23

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Residues: 257864 seqs, 26547834 residues

Total number of hits satisfying chosen parameters: 257454

Maximum hit seq length: 0

Maximum hit seq length: 20000000

Best processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database	Length	Parent's AA Now	
1	23	ISLERASLTGTHAVRAVRLSST	New Comp Rep
2	23	ISLERASLTGTHAVRAVRLSST	New Comp Rep
3	23	ISLERASLTGTHAVRAVRLSST	New Comp Rep
4	23	ISLERASLTGTHAVRAVRLSST	New Comp Rep
5	23	ISLERASLTGTHAVRAVRLSST	New Comp Rep
6	23	ISLERASLTGTHAVRAVRLSST	New Comp Rep
7	23	ISLERASLTGTHAVRAVRLSST	New Comp Rep

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Prod. No.	Score	Match	Length	DB	16	Description
1	47	43.1	97	1	PCT-US02-32727-1266	Sequence 1266, Ap
2	47	43.1	97	6	US-10-057-498-1266	Sequence 1266, Ap
3	47	43.1	627	1	PCT-US02-32727-12775	Sequence 12775, A
4	47	43.1	627	6	US-10-057-498-12775	Sequence 12775, A
5	44.5	40.8	136	5	US-09-724-676-82654	Sequence 82654, A
6	44.5	40.8	136	5	US-09-724-676-82654	Sequence 82654, A
7	44.5	40.8	362	5	US-09-724-676-82629	Sequence 82629, A
8	44.5	40.8	362	5	US-09-724-676-82645	Sequence 82645, A
9	44.5	40.8	362	5	US-09-724-676-82629	Sequence 82629, A
10	44.5	40.8	362	5	US-09-724-676-82645	Sequence 82645, A
11	44.5	40.8	418	5	US-09-724-676-82637	Sequence 82637, A
12	44.5	40.8	418	5	US-09-724-676-82637	Sequence 82637, A
13	44.5	40.8	418	5	US-09-724-676-82637	Sequence 82637, A
14	44.5	40.8	418	5	US-09-724-676-82637	Sequence 82637, A
15	42	38.5	99	1	PCT-US02-32727-9326	Sequence 9326, Ap
16	42	38.5	99	6	US-10-057-498-9326	Sequence 9326, Ap
17	41	37.6	124	1	PCT-US02-32727-10546	Sequence 10546, A
18	41	37.6	124	6	US-10-057-498-10546	Sequence 10546, A
19	41	37.6	364	1	PCT-US02-33645-27	Sequence 27, Appl
20	41	37.6	439	5	US-09-134-0067-4641	Sequence 4641, Ap
21	41	37.6	439	5	US-09-134-0067-4641	Sequence 4641, Ap
22	40	36.7	59	1	PCT-US02-32727-7611	Sequence 7611, Ap
23	40	36.7	59	6	US-10-057-498-7611	Sequence 7611, Ap
24	40	36.7	115	1	PCT-US02-32727-3074	Sequence 3074, Ap
25	40	36.7	115	6	US-10-057-498-3074	Sequence 3074, Ap
26	40	36.7	251	5	US-09-134-0067-3430	Sequence 3430, Ap

ALIGNMENTS

RESULT 1  
PCT-US02-32727-1266  
; Sequence 1266, Application: PCT/US02/32727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yashir  
; APPLICANT: Persing, David  
; APPLICANT: Bhattacharya, Ajay  
; APPLICANT: Bhattacharya, Jean-Francois  
; APPLICANT: Chang, Yuhui  
; APPLICANT: Wang, Shiqin  
; APPLICANT: Wang, Shiqin  
; APPLICANT: Godes, Michael  
; APPLICANT: Benson, Brian  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Patrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglas, John  
; APPLICANT: Douglas, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICANT OR REFERENCE: PCT/US02/32727  
; CURRENT FILING DATE: 2002 10 11  
; NUMBER OF SEQ ID NOS: 40942  
; SEQ ID NO 1266  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Propionibacterium

PCT-US02-32727-1266  
Query Match 43.1% Score 172 Length 97  
Best Local Similarity 43.1% Prod. No. 13  
Mat. No. 9, Mismatches 6, Indels 0, Gaps 0

US 10 057-498 1266  
; Sequence 1266, Application US/10057498  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yashir  
; APPLICANT: Persing, David  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne  
; FILE REFERENCE: 210121.514  
; CURRENT APPLICANT OR REFERENCE: PCT/US02/32727  
; CURRENT FILING DATE: 2002 10 11







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CompuGen version 5.1.1.3

EM protein protein search, using sw model

Run on: January 2, 2003, 12:26:31 : Search time 6.2 seconds  
(without alignments)  
69,097 Million cell updates/sec

Profile: 03 09 786 317 2

Profile score: 100

Sequence: 1 LSTAFVAVLHGHVFAVRLKSL 23

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 9

Maximum DB seq length: 239999999

Post processing: Maximum Match 100%

Maximum Match 100%

List first 45 summaries

Database: PIR 73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	LR	LR	Description
1	65	59.6	1906	1	563235	myosin-light-chain
2	58	53.2	1147	2	53337	myosin-light-chain
3	58	53.2	1176	2	38393	myosin-light-chain
4	47	45.7	237	2	393420	sugar phosphate m
5	47	45.1	333	2	33285	cysteine proteinase
6	47	45.1	464	2	382517	hypothetical prote
7	47	45.1	597	2	382566	hypothetical prote
8	46	42.2	456	2	397296	UDP-N-acetylglucos
9	46	41.3	96	2	34708	immunoreactive epi
10	46	41.3	143	2	382321	hypothetical prote
11	46	41.3	237	2	325214	hypothetical prote
12	46	41.3	360	2	372591	probable sugar pho
13	46	41.3	457	2	383178	signal recognition
14	44	40.4	452	2	335762	hypothetical prote
15	44	40.4	458	2	375375	probable amino aci
16	44	40.4	598	2	375626	PLS system, fructo
17	43	39.4	233	2	384237	hypothetical prote
18	43	39.4	315	2	383567	permease imported
19	43	39.4	324	1	196135	transforming prote
20	43	39.4	398	2	382554	conserved hypothet
21	43	39.4	457	2	376009	hypothetical prote
22	43	39.4	477	2	383205	streptolysin C (b
23	43	39.4	544	2	383775	probable lyase IAS
24	43	39.4	883	2	379879	hypothetical prote
25	43	39.4	133	2	383516	probable ftsK My
26	42	38.5	225	2	384377	glucose 5-phosphate
27	42	38.5	455	2	383558	UDP-N-acetylglucos
28	42	38.5	458	2	386860	hypothetical prote

30	42	38.5	501	2	383614	succinylglutamic bios
31	42	38.5	706	2	309699	bib protein-trim
32	42	38.5	1159	2	115965	hypothetical prote
33	41.5	38.1	299	2	382393	transcription requ
34	41.5	38.1	456	2	381244	UDP-N-acetylglucos
35	41	37.6	116	2	375566	hypothetical prote
36	41	37.6	195	2	398268	hypothetical 21.1K
37	41	37.6	195	2	383015	5-formyltetrahydro
38	41	37.6	202	2	149634	hypothetical prote
39	41	37.6	243	2	171458	hypothetical prote
40	41	37.6	355	2	390165	hypothetical prote
41	41	37.6	357	2	369122	conserved hypothet
42	41	37.6	359	2	126342	hypothetical prote
43	41	37.6	379	2	132294	probable cathepsin
44	41	37.6	462	2	387564	UDP-N-acetylglucos
45	41	37.6	476	2	135761	probable monooxygen

ALIGNMENTS

RESULT 1

S68235

myosin light chain kinase (E: 217,1117), 210K, nonmuscle chicken

N: Contains: myosin light chain kinase, 100K, smooth muscle; telokin

C: Species: Gallus gallus (chicken)

C: Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext change 10-Sep-1999

C: Accession: S68235; A37099; I44389; A43389; S28227; S78216; A36993; A29810; S11652

R: Watterson, D.M.; Collinge, M.; Lukas, T.J.; Van Eldik, L.J.; Krukow, K.G.; Stepano

FERS Lett. 373, 217-220, 1995

A: Title: Multiple gene products are produced from a novel protein kinase transcription

A: Reference number: S68235; MIM:96033976; PMID:7589469

A: Accession: S68235

A: Status: nucleic acid sequence not shown

A: Molecule type: mRNA

A: Residues: 1-1906, 5W1P

A: Cross-references: EMBL:X12876; NID:992992; PIR:N:AA47056.1; PDB:992993

K: Shoemaker, M.; Lee, W.; Sotter, W.; Kwiatkowski, A.P.; Matrisian, P.E.; Quert

J. Cell Biol. 111, 1107-1125, 1990

A: Title: Use of DNA sequence and mutant analyses and antisense oligodeoxynucleotides

activity.

A: Reference number: A37099; MIM:96033976; PMID:2362734

A: Accession: A37099

A: Molecule type: mRNA

A: Residues: 649-1906, 5S8S

A: Cross-references: EMBL:X52876

K: Collinge, M.; Matrisian, P.E.; Zimmer, W.E.; Shattuck, R.L.; Lukas, T.J.; Van Eldik

Mol. Cell. Biol. 12, 2359-2371, 1992

A: Title: Structure and expression of a calcium binding protein gene contained within

A: Reference number: A44389; MIM:92236611; PMID:1373815

A: Accession: A44389

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1695-1906, 5C0L

A: Cross-references: GB:BB8284; NID:321237; PIR:AA85767.1; PDB:212238

A: Accession: A44389

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 1750-1906, 5C02

A: Cross-references: GB:BB8283; NID:321137; PIR:AAA48647.1; PDB:211372

K: Yoshikata, S.; Ikeda, M.

Arch. Biochem. Biophys. 299, 242-247, 1992

A: Title: Molecular cloning of the chicken giant telokin gene and cDNA.

A: Reference number: S28227; MIM:96033972; PMID:1444362

A: Accession: S28227

A: Molecule type: mRNA

A: Residues: 1750-1906, 5Y0S

A: Cross-references: EMBL:M96655; NID:321234; PIR:AAA49083.1; PDB:212745

A: Accession: S28227

A: Molecule type: DNA

A: Residues: 1750-1906, 5Y0W

A: Cross-references: EMBL:M96687

R: Johnson, N.J.; Portson, R.B.; Nedelmann, G.S.; Barkley, M.Y.; Kemp, B.E.; Means, A.R.



Proc. Natl. Acad. Sci. U.S.A. 87, 2284-2288, 1990  
 A:Title: Regulatory and structural motifs of chicken gizzard myosin light chain kinase  
 A:Accession: A59407  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 935-1438, 1077-1440-1906 <GAL>  
 A:Cross references: GB:M31048; NID:4212660; PDB:AAA49069.1, PDB:4212661  
 R:Cherrier J., V. Russo, M.A. Gilson, N.J. Putkey, J.A. Young, A.R. Biochemistry 25, 8372-8381, 1986  
 A:Title: Domain organization of chicken gizzard myosin light chain kinase deduced from a  
 A:Reference number: A25810; MUID:87157587; PMID:3030394  
 A:Accession: A25810  
 A:Molecule type: mRNA  
 A:Residues: 1259-1439, 1077-1440-1906 <GUE>  
 C:Genetics: 7  
 C:Supertfamily: myosin-light-chain kinase, nonmuscle, fibronectin type III repeat homology  
 C:Keywords: alternative initiators; ATP; calmodulin binding; phosphoprotein; phosphotransferase  
 F:542-599/Region: immunoglobulin homology <IMM>  
 F:935-1906/Region: myosin-light-chain kinase, 108K, smooth muscle (from 5.5kb transcrip  
 F:1063-1153/Region: immunoglobulin homology <IMM>  
 F:1451-1708/Region: protein kinase homology <KIN>  
 F:1459-1467/Region: protein kinase ATP binding motif  
 F:1750-1906/Region: protein kinase related protein RFP (from 2.7 kb transcrip) <SLA  
 F:1808-1869/Region: immunoglobulin homology <IMM>

Query Match 59.6% Score 65; DB 1; Length 1906;  
 Best Local Similarity 78.9%; Pred. No. 0.87;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 PRASLCQCHAVAVATGRSS 22

DB 1731 PRKWKQKTGNVAVATGRSS 1736

RESULT 2

A59407  
 myosin-light chain kinase (EC 2.7.1.117), smooth muscle rabbit  
 C:Date: 20 Jun 2000 #sequence\_revision 20 Jun 2000 #text\_change 20 Jun 2000  
 C:Accession: A59407; A41674; B41674; A40210  
 R:Gallagher, P. J. Herring, R. P. Griffin, S. A. Stull, J. T. J. Biol. Chem. 266, 23936-23944, 1991  
 A:Title: Molecular characterization of a mammalian smooth muscle myosin light chain kinase  
 A:Reference number: A41674; MUID:92084694; PMID:1748666  
 A:Accession: A59407  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <GAL>  
 A:Cross references: GB:M76233, NID:4165703, PDB:AAA73093.1, PDB:4165704  
 A:Experimental source: dev stane Adult, sex Female, tissue type smooth muscle  
 A:Note: this revision submission is not cited in GenBank entry FARSMMICKE, release 115  
 A:Accession: A41674  
 A:Molecule type: mRNA  
 A:Residues: 1748-1749, 1741-1147 <GAT>  
 A:Cross-reference: GB:M76233  
 A:Note: the sequence is revised in GenBank entry FARSMMICKE, release 115. (PDB:AAA73093)  
 A:Accession: B41674  
 A:Molecule type: DNA  
 A:Residues: 1-22, 127-129, 129-130  
 A:Cross-references: GB:M76369  
 A:Note: this translation is not annotated in GenBank entry FARSMMICKE, release 115  
 A:Note: this sequence has been revised in reference A40210  
 R:Gallagher, P. J., Herring, R. P., Griffin, S. A., Stull, J. T. J. Biol. Chem. 267, 9450-9452, 1992  
 A:Reference number: A40210; MUID:92259555; PMID:1577772  
 A:Contents: erratum  
 A:Accession: A40210  
 A:Molecule type: DNA  
 A:Residues: 21-40 <GAT>  
 A:Note: this is a revision to the sequence B41674 from reference A41674  
 C:Supertfamily: unclassified subfamily of type specific protein kinases; fibronectin type III

C:Keywords: ATP; phosphotransferase; smooth muscle  
 F:417-469/Region: protein kinase homology <IMM>  
 F:651-952/Region: protein kinase homology <IMM>  
 F:702-710/Region: protein kinase ATP-binding motif  
 F:1055-1116/Region: immunoglobulin homology <IMM>

Query Match 52.2% Score 59; DB 2; Length 1147;  
 Best Local Similarity 73.7%; Pred. No. 0.67;  
 Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 PRASLCQCHAVAVATGRSS 22

DB 974 PRKWKQKTGNVAVATGRSS 992

RESULT 3

A50583  
 myosin light chain kinase (EC 2.7.1.117) 155K protein - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 23 Feb 1994 #sequence\_revision 23 Feb 1994 #text\_change 20 Apr 2000  
 C:Accession: JN0583; PN0490  
 R:Kobayashi, H., Inoue, A., Mikawa, T., Kawayama, M., Motoki, Y., Masaki, T., Ebashi, Y. Biochem. 117, 786-791, 1992  
 A:Title: Isolation of cDNA for bovine smooth muscle myosin light chain kinase  
 A:Reference number: JN0583; MUID:92092149; PMID:1394347  
 A:Accession: JN0583  
 A:Molecule type: mRNA  
 A:Residues: 1-1176 <KOR>  
 A:Cross references: GB:S57131, NID:4298638, PDB:AA25794.1; PDB:4298639  
 A:Experimental source: stomach  
 A:Accession: PN0490  
 A:Molecule type: protein  
 A:Residues: 44-55; 721-728; 828-851; 1002-1019 <KOR>  
 C:Keywords: ATP; calmodulin binding; phosphotransferase  
 F:370-430/Region: immunoglobulin homology <IMM>  
 F:723-940/Region: protein kinase homology <KIN>  
 F:731-739/Region: protein kinase ATP-binding motif  
 F:1090-1144/Region: immunoglobulin homology <IMM>

Query Match 52.2% Score 59; DB 2; Length 1176;  
 Best Local Similarity 73.7%; Pred. No. 0.68;  
 Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 PRASLCQCHAVAVATGRSS 22

DB 1003 PRKWKQKTGNVAVATGRSS 1021

RESULT 4

A99420  
 sugar phosphate nucleotidyl transferase [imported] - Sulfolobus solfataricus  
 C:Species: Sulfolobus solfataricus  
 C:Date: 24 May 2001 #sequence\_revision 24 May 2001 #text\_change 24 May 2001  
 C:Accession: A99420  
 R:Shao, Q., Singh, E. K., Gelfandberg, E., Zivanovic, V., Allard, G., Arayata, M. J., Ch. J. Biol. Chem. 276, 11111-11117, 2001  
 A:Title: Purification and characterization of the sugar phosphate nucleotidyl transferase from Sulfolobus solfataricus  
 A:Reference number: A99420  
 A:Accession: A99420  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-237 <KOR>  
 A:Cross references: GB:AA096641; MUID:41915781; PDB:AAK42616.1; GSPDB:GN00155  
 C:Genetics: 1  
 A:Gene: SS02479

Query Match 45.0% Score 49; DB 2; Length 237;  
 Best Local Similarity 50.0%; Pred. No. 3.6;  
 Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;



QY 2 SLRRASLSLGTGHAVR 15  
| | | | |  
DB 71 SLQSEQLGTGHAVR 84

## RESULT 9

B45708

Immunoreactive epitope (clone A14) - human astrovirus (fragment)

C:Species: human astrovirus

C:Date: 21-Sep-1993 #sequence\_revision 18 Nov 1994 #text\_change 08-Oct-1999

C:Accession: B45708

R:Matsumi, S.M.; Kim, J.P.; Greenberg, H.B.; Young, L.M.; Smith, L.S.; Lewis, T.L.; Herrin

J. Virol. 67, 1712-1715, 1994

A:Title: Cloning and characterization of human astrovirus immunoreactive epitopes.

A:Reference number: A45708; MIM:03172368; PMID:7679752

A:Accession: B45708

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 &lt;MAI&gt;

A:Cross-references: GB:108015; NID:q225421; PIDN:AAA40213.1; PID:q225422

A:Experimental source: serotype 1

A:Note: sequence extracted from NCBI backbone (NCBI:125392, NCBI:125384)

Query Match 41.3%; Score 45; DB 2; Length 96;

Best Local Similarity 52.6%; Pred. No. 6.3;

Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 TSLRRASLSLGTGHAVRAIGR 19

| | | | |

DB 11 TQMNPQLSGHGEAPAAIGR 29

## RESULT 10

A82321

Hypothetical protein VC0457 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence\_revision 20 Aug 2000 #text\_change 02 Feb 2001

C:Accession: A82321

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Charidson, P.; Ermolacova, M.B.; Vamathevan, J.; Bass, S.; Olin, B.; Staudo, T.; Sellers, R

L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-484, 2000

A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82045; MIM:20406933; PMID:10952201

A:Accession: A82321

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-143 &lt;HEI&gt;

A:Cross-references: GB:AE004132; GB:AE003852; NID:q9654871; PIDN:AAF93630.1; GSPDB:GN001

A:Experimental source: serogroup O1, strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0457

A:Map position: 1

Query Match

Best Local Similarity 41.3%; Score 45; DB 2; Length 143;

Matches 13; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

QY 3 LRRASLSLGTGHAVRAIGRL 20

| | | | |

DB 64 LDRASLKPATPAKLTGHAKNLICNL 89

## RESULT 11

B75214

Hypothetical protein PAR0160 - Pyrococcus abyssi (strain orsay)

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jan-2000

C:Accession: B75214

R:Anonymous; Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence. Insights into archaeal chromosome stru

A:Reference number: A75001

A:Accession: B75214

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 &lt;KAW&gt;

A:Cross-references: GB:AJ248283; GB:AL096836; NID:q5457433; PIDN:GAB49131.1; PID:q545

A:Experimental source: strain orsay

C:Genetics:

A:Gene: PAR0160

C:Superfamily: hypothetical protein M10933

Query Match

Best Local Similarity 41.3%; Score 45; DB 2; Length 237;

Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 TETPPASLGTGHAVRAIGRL 20

| | | | |

DB 142 INFERRAKVGESGAVSSVGEI 161

## RESULT 12

F72591

Probable sugar phosphate transferase APPL202 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence\_revision 20 Aug 1999 #text\_change 20-Aug-1999

C:Accession: F72591

R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Maikawa, Y.; Jin-no, K.; Ta

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyperthermophilic Crenarchaeon, Aero

A:Reference number: A72450; MIM:09910429; PMID:1092966

A:Accession: F72591

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-360 &lt;KAW&gt;

A:Cross-references: GB:AF000065; NID:q510462; PIDN:KAA03138.1; PID:dl043974; PID:q

A:Experimental source: strain K1

C:Genetics:

A:Gene: APPL202

Query Match

Best Local Similarity 41.3%; Score 45; DB 2; Length 360;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 SLGTGHAVRAI 17

| | | | |

DB 28 ALGTGHAVRRV 38

## RESULT 13

F83178

Signal recognition particle protein Pih PA3746 [imported] - Pseudomonas aeruginosa (s

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 03-Jun-2002

C:Accession: F83178

R:Storer, G.K.; Pham, X.Q.; Brink, A.L.; Mitsuuchi, C.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Reilly, L.L.; Gatter, G.N.; Palmer, P.W.; Kay, A.; Jarboe, P.; L

J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MIM:20447337; PMID:10984043

A:Accession: F83178

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-457 &lt;STO&gt;

A:Cross-references: GB:AF004793; GB:AF004091; NID:q9949904; PIDN:AA007133.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: Pih; PA3746

C:Superfamily: signal recognition particle 54K protein

Query Match

Best Local Similarity 41.3%; Score 45; DB 2; Length 457;

Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

27 4 PRASLSTGHAVRAIGRL 20  
1 1111 11111  
db 4-4 PRASLSTGHAVRAIGRL 419

PROTEIN 14

14762

Probable amino acid decarboxylase - Streptomyces coelicolor

Species: Streptomyces coelicolor

Clade: 05 Nov 1999 #sequence\_revision 05 Nov 1999 #taxi\_change 21-Jan-2000

Accession: U5762

Submitters: G. Harris, D. Bentley, S.D. Parkhill, J. Barrell, B.G. R. Jandreadu, M.

Submitted to the EMBL Data Library, August 1999

Accession number: Z1588

Accession: U5762

Annotation: preliminary; translated from db/EMBL/Uncl

Accession type: DNA

Accession: U5762 - SAIL

Accession references: EMBL:AL10732; FIDN:AB52073.1; GSIIDB:GN00070; SCOEIDB:SC7H2.31c

Experimental source: strain A5(2)

Comments:

Accession: SCOEIDB:SC7H2.31c

Superfamily: human glutamate decarboxylase

Query Match 40.44; Score 44; DB 2; Length 452;

Best Local Similarity 56.56; Pred. No. 42;

Matches 15; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

27 2 SLRRASLSTGHAV RAIGRL 20  
1 1111 11111  
db 4-4 AVPRALSTGHAVRAIGRL 423

PROTEIN 15

376376

Hyperthermophilic protein 376376 - Sulfolobus solfataricus

Species: Sulfolobus solfataricus

Clade: 09 Oct 1997 #sequence\_revision 24 Oct 1997 #taxi\_change 17-Mar-1999

Accession: S75376

Submitters: W. Klenk, R.P. Singh, R.K. Allard, G. Chan, C.C.Y. Liu, D.Y. Penny, S.

Microbiol. 22, 175-191, 1996

Submitted to the EMBL Data Library and information content of an archael genome;

Accession number: S73076; MIMD:97055432; PMID:8899719

Accession: S75376

Annotation: nucleic acid sequence not shown; translation not shown

Accession type: DNA

Accession: U5762 - SAIL

Accession references: EMBL:Y8257; NIDB:173772; PIR:284974; FIDN:1767780

Experimental source: strain P2

Accession: The nucleotide sequence was submitted to the EMBL Data Library, September 1996

Query Match 40.44; Score 44; DB 2; Length 458;

Best Local Similarity 56.16; Pred. No. 43;

Matches 16; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

27 2 SLRRASLSTGHAVRAIGRL 22  
1 1111 11111  
db 4-4 SARRSSTGHAVRAIGRL 474

Search completed: January 2, 2003, 12:29:18

Job time: 3.00 secs



GenPro version 5.1.1.3  
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QM protein protein search using sw model

Run on: January 2, 2003, 12:26:31 ; Search time 7 seconds  
(without alignments)  
136.27% BLAST from all updates/seqs

Query: ES\_09\_786\_317\_2  
Perfect score: 199  
Sequence: 1 FSLPRASSTGTHAVRAVAGLSS( 23)

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searches: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 250000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length DB	ID	Description
1	65	59.6	1006	1 KMLS_CHICK	P11799 galpus gall
2	58	53.2	438	1 KMLS_SHEEP	Q92927 ovic aricg
3	58	53.2	1147	1 KMLS_RABIT	P29294 ovicolaqus
4	58	53.2	1176	1 KMLS_BOVIN	Q28824 bovs taurus
5	58	53.2	1914	1 KMLS_HUMAN	Q15746 homo sapien
6	43	39.4	424	1 MAS_RAT	P12526 rattus norv
7	43	39.4	457	1 PEP1_SHEEP	P52329 streptomyce
8	42	38.5	700	1 B1B_DROME	P25645 drosophila
9	41.5	38.1	456	1 G1M1_NEIGH	Q50986 molisseria q
10	41	37.6	537	1 KICA_MELPH	Q27937 methanobact
11	41	37.6	479	1 P1B6_CAFEL	P43510 caenorhabdi
12	41	37.6	664	1 ALGX_PICAN	P64941 picidia amp
13	41	37.6	635	1 PMA1_CANAL	P28877 candida alb
14	41	37.4	1479	1 ALA1_CANAL	Q13368 candida alb
15	41	37.6	1499	1 A100_HUMAN	Q60312 homo sapien
16	40	36.7	306	1 RF1_ARABE	Q8YPK9 arabidra sp
17	40	36.7	483	1 C311_DROME	Q9VY97 drosophila
18	40	36.7	534	1 S1K1_YEAST	Q12460 saccharomye
19	40	36.7	578	1 V1PC_SALTI	Q04975 salmonella
20	40	36.7	609	1 Y4FA_RHUSN	P55610 rhizobium s
21	40	36.7	823	1 ENL1_TREPA	Q84642 trepocoma p
22	40	36.7	1019	1 ENIK_HUMAN	P98073 homo sapien
23	40	36.7	1582	1 YU40_RALSC	Q8X202 ralistonia s
24	40	36.7	3034	1 C1R1_MOUSE	Q35161 mus musculu
25	39.5	35.2	483	1 NDAD_ALGXY	P72349 alchidomene
26	39	35.8	48	1 D4_1_PSEPO	P00881 pseudomonas
27	39	35.8	131	1 FABB_BOVIN	Q09139 bos taurus
28	39	35.8	132	1 FABB_BOVIN	P10790 bos taurus
29	39	35.8	132	1 N1KP_BOVME	Q8Y7P2 bruceella me
30	39	35.8	132	1 N1KP_BOVME	Q9A183 bruceella sa
31	39	35.8	134	1 PR9_GOUTH	P19459 quillardia
32	39	35.8	245	1 K14_JENHI	Q15594 entamoeba h
33	39	35.8	276	1 PRX2_XYRYZ	Q55521 syncytocyst

ALIGNMENTS

RESULT 1

KMLS\_CHICK

ID KMLS\_CHICK STANDARD; PRT: 1906 AA;

AC P11799; P19038;

DT 01-oct-1989 (Ref. 12, created)

DT 01-oct-1996 (Ref. 34, last sequence update)

DT 15 JUN-2002 (Ref. 41, last annotation update)

DE Myosin light chain kinase, smooth muscle and non muscle isoforms

DE (EC 2.7.1.117) (MCK) [Ontario: telekin]

OS Gallus gallus (chicken)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus

OX NCBI\_TaxID: 9031;

RN 111

RP SEQUENCE FROM N.A. (MCK 210)

RX MEDLINE 96033976; PubMed 7689469;

RA Watterson D.M., Collins M., Lukas L., van Eldik L., Kirilov K.G.,

RA Stepanova O.V., Shirinsky V.P.

RT "Multiple gene products are produced from a novel protein kinase

RT transcription region."

RL FEBS Lett. 373:217-220(1995).

RN 121

RP SEQUENCE FROM N.A. (MCK 108)

RX MEDLINE 9012792; PubMed 2315429;

RA Olson N.J., Pearson R.B., Needleman P.S., Horwitz M.L., Kemp B.E.,

RA Means A.R.

RT "Regulatory and structural motifs of chickenizzard myosin light

RT chain kinase."

RL Proc. Natl. Acad. Sci. U.S.A. 87:2284-2288(1990).

RN 131

RP SEQUENCE OF 645 1986 FROM N.A. AND PABIAL SEQUENCE.

RC TISSUE Fibroblast;

RX MEDLINE 90361748; PubMed 2202744;

RA Shemakier M., Lee W., Chivark P.L., Kwiatkowski A.P.,

RA Marislian P.E., Guerra Santos L., Wilson R., Lukas L.,

RA van Eldik L.J., Watterson D.M.

RT "Use of DNA sequence and mutant analyses and antisense

RT oligodeoxynucleotides to examine the molecular basis of nonmuscle

RT myosin light chain kinase autoinhibition, calmodulin regulation, and

RT activity."

RL J. Cell Biol. 111:1107-1125(1990).

RN 141

RP SEQUENCE OF 1259 1986 FROM N.A.

RC TISSUE-Gizzard;

RX MEDLINE 87157587; PubMed 3000047;

RA Guerrero I., Jr., Russo M.A., Olson N.J., Kirilov K.G., Means A.R.

RT "Genin organization of chickenizzard myosin light chain kinase

RT deduced from a cloned cDNA."

RL Biochemistry 25:8372-8381(1986).

RN 151

RP SEQUENCE OF 1750 1986 FROM N.A. (MCK108)

RC TISSUE-Gizzard;

RX MEDLINE 93073972; PubMed 1444462;

RA Yoshikai S., Ikeda M.

RT "Molecular cloning of the chicken gizzard chicken gizzard cDNA."

Arch. Biochem. Biophys. 299:242-247(1992).  
 16.  
 RN SEQUENCE: F 1750 1996 FROM N.A. (TELOKIN).  
 RX MEDLINE 9224611; PubMed 1272915;  
 RA Collinge M., Matrisian P.E., Simmer W.E., Shattuck R.L., Lukas T.J.,  
 KA van Blisk W.J., Waterson D.M.;  
 "Structure and expression of a calcium-binding protein gene contained  
 within a calmodulin-regulated protein kinase gene.";  
 RL Mol. Cell. Biol. 12:2459-2471(1992).  
 CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A  
 MYOSIN LIGHT CHAIN, WHICH LEADS TO THE FORMATION CALMODULIN/  
 MUCK SIGNAL TRANSDUCTION COMPLEXES WHICH ALLOW SELECTIVE  
 TRANSDUCTION OF CALCIUM SIGNALS.  
 CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] - ADP + [myosin  
 light-chain] phosphate.  
 CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms, MUCK-210/non muscle  
 form, MUCK-108/smooth muscle form and telokin; are  
 produced by alternative initiation.  
 CC -1- TISSUE SPECIFICITY: TELOKIN IS EXPRESSED IN GIZZARD, HEART, LUNG,  
 INTESTINE, AND SKELETAL MUSCLE ALTHOUGH THE LEVELS OF THE  
 EXPRESSION IN THE LATTER WERE MUCH HIGHER THAN THAT IN THE GIZZARD.  
 CC -1- DOMAIN: TELOKIN BINDS CALMODULIN.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN LIKE C2 TYPE DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
 -----  
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 or send an email to [license@isb.sib.ch](mailto:license@isb.sib.ch)).  
 -----  
 DR EMBL: X52876; CAA37056.1; -;  
 DR EMBL: X52876; CAA37057.1; -;  
 DR EMBL: X52876; CAA37058.1; -;  
 DR EMBL: M31048; AAA49069.1; -;  
 DR EMBL: M14953; AAA69964.1; -;  
 DR EMBL: M96655; AAA49083.1; -;  
 DR EMBL: M88283; AAA48647.1; -;  
 DR EMBL: M88284; AAB53768.1; -;  
 DR PIR: A25810; A25810.  
 DR PIR: A37099; A37099.  
 DR PIR: S11652; S11652.  
 DR HSSP: P56276; TLTK.  
 DR InterPro: IPR000779; Euk\_pkinase.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003006; Iq\_MHC.  
 DR InterPro: IPR003598; Iq\_C2.  
 DR InterPro: IPR003600; Iq\_Like.  
 DR InterPro: IPR022990; Ser\_thr\_pkinase.  
 DR Pfam: PF00041; tn3; 1.  
 DR Pfam: PF00047; Iq; 9.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00060; FN3; 1.  
 DR SMART: SM00410; Iq\_Like; 1.  
 DR SMART: SM00408; Iq\_C2; 8.  
 DR SMART: SM00220; SLTK; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferrase: Serine/threonine protein kinase; Calmodulin binding;  
 KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;  
 KW Alternative initiation.  
 FT CHAIN 1 1906 MYOSIN LIGHT CHAIN KINASE, MUCK-210 (NON-  
 FT MUSCLE ISOZYME).  
 FT CHAIN 935 1906 MYOSIN LIGHT CHAIN KINASE, MUCK 108  
 FT (SMOOTH-MUSCLE ISOZYME).  
 FT CHAIN 1750 1906  
 FT INIT\_MET 935 935 FOR MUCK 108.  
 FT INIT\_MET 1750 1750 FOR TELOKIN.

FT DOMAIN 1310 1400 FIBRONECTIN TYPE-III  
 FT DOMAIN 1453 1708 PROTEIN KINASE.  
 FT DOMAIN 1899 1970 IG-LIKE C2 TYPE DOMAIN.  
 FT NP\_BIND 1459 1467 ATP (BY SIMILARITY).  
 FT BINDING 1482 1482 ATP (BY SIMILARITY).  
 FT ACT\_SITE 1574 1574 BY SIMILARITY.  
 FT DOMAIN 1716 1728 CALMODULIN AUTOINHIBITION (AR15) REGION  
 FT (POTENTIAL).  
 FT DOMAIN 1740 1749 CALMODULIN RECOGNITION (RS20) REGION  
 FT (POTENTIAL).  
 FT DOMAIN 1317 1364 MOTIF 1A.  
 FT DOMAIN 1385 1402 MOTIF 1B.  
 FT DOMAIN 660 1833 4 X REPEATS, MOTIF 11A.  
 FT REPEAT 660 676 11A-1.  
 FT REPEAT 758 774 11A-2.  
 FT REPEAT 1107 1123 11A-3.  
 FT REPEAT 1817 1833 11A-4.  
 FT DOMAIN 693 1866 5 X REPEATS, MOTIF 11B.  
 FT REPEAT 693 708 11B-1.  
 FT REPEAT 791 807 11B-2.  
 FT REPEAT 1140 1156 11B-3.  
 FT REPEAT 1281 1297 11B-4.  
 FT REPEAT 1851 1866 11B-5.  
 FT DOMAIN 970 1226 4 X REPEATS, MOTIF 11C.  
 FT REPEAT 970 987 11C-1.  
 FT REPEAT 999 1016 11C-2.  
 FT REPEAT 1061 1078 11C-3.  
 FT REPEAT 1209 1226 11C-4.  
 FT DOMAIN 1700 1763 CALMODULIN-BINDING.  
 FT DOMAIN 1896 1906 POLY-GLU.  
 FT MOD\_RES 1748 1748 PHOSPHORYLATION.  
 FT MOD\_RES 1756 1756 PHOSPHORYLATION.  
 FT CONFLICT 1439 1439 R -> Q (IN REF. 4).  
 SQ SEQUENCE 1906 AA; 210445 MW; AD7D8A1B69FF3363 CRC64;  
 Query Match 59.6%; Score 65; DB 1; Length 1906;  
 Best Local Similarity 78.9%; Pred. No. 0.03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 RRASLGTGHAVRAIGRLSS 22  
 II |||||  
 DB 1731 RRKWKGTGHAVRAIGRLSS 1749  
 RESULT 2  
 KMLS\_SHEEP STANDARD; PRT: 438 AA.  
 ID KMLS\_SHEEP  
 AC 002827;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, last sequence update)  
 DT 16 OCT 2001 (Rel. 40, last annotation update)  
 LE Myosin light chain kinase, smooth muscle (E1 237,1117) (MUSE)  
 DE [Contains: Telokin] (Fragment).  
 GN MYLK.  
 OS ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Ruminantia; Cetartiodactyla; Bovidae; Bovinae;  
 OC Bovidae; Caprinae; Ovis.  
 NX NCPI\_TaxID 9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 96129379; PubMed 8569750;  
 RA Pato M.D., Kerc E., Lye S.J.;  
 FT "Phosphorylation and partial sequence of pregnant sheep myometrium  
 myosin light chain kinase.";  
 RL Mol. Cell. Biochem. 149:59-65(1995).  
 CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A  
 MYOSIN LIGHT CHAIN.  
 CC -1- CATALYTIC ACTIVITY: ATP + [myosin light chain] - ADP + [myosin  
 light chain] phosphate.  
 CC ! DOMAIN: TELOKIN BTHDS CALMODULIN.  
 CC ! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.



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DR EMBL: 303667; AAA02110.2;  
DR BSSP: P56276; 11LK;  
DR InterPro: IPR000719; Pak\_kinase;  
DR InterPro: IPR000066; Iq\_MBP;  
DR InterPro: IPR000598; Iq\_c2;  
DR InterPro: IPR002290; Ser\_thr\_kinase;  
DR Pfam: PF00069; PKinase; 1;  
DR Pfam: PF00047; Iq; 1;  
DR Pfam: PF00001; Pak\_kinase; 1;  
DR SMART: SM00408; Iq\_c2; 1;  
DR SMART: SM00408; Iq\_c2; 1;  
DR PROSITE: PS00107; PROTEIN\_KINASE\_AIP; PARTIAL;  
DR PROSITE: PS00108; PROTEIN\_KINASE\_S1; 1;  
DR PROSITE: PS00117; PROTEIN\_KINASE\_PPM; 1;  
KW Transferrase; Serine/threonine protein kinase; Calmodulin-binding;  
KW AIP binding; Phosphorylation; Immunoglobulin domain;  
FT NEW DEF 1  
FT DOMAIN 1 241 PROTEIN KINASE;  
FT DOMAIN 243 296 CALMODULIN BINDING;  
FT DOMAIN 346 413 IQ-LIKE C2 TYPE DOMAIN;  
FT BINDING 15 15 AIP (BY SIMILARITY);  
FT ACT\_SITE 107 107 BY SIMILARITY;  
FT DOMAIN 203 436 TELOKIN;  
FT DOMAIN 433 436 POLY GLU;  
SQ SEQUENCE 438 AA; 49503 MW; 77A02F4886A10B51 CRef64;

Query Match: 64.2%; Score 59; 103 17; Length 438;  
Best Local Similarity: 74.7%; Pred. Res. 6094;  
Matches: 14; Conservatize 1; Mismatches 4; Indels 0; Gaps 0;

27 4 REASSEMBLY:NAVAFAIGRESS 22  
11 111111111111  
16 264 PRKWKRTGNAVAFAIGRESS 262

PROTEIN 4  
KM33 RAB11  
ID KM33 RAB11 STANDARD; PRT; 1147 AA.  
AC P29294; Q28729;  
DI 01 DEC 1992 (Ref. 24; Created)  
DI 15 JUL 1998 (Ref. 36; Last sequence update)  
DI 16 OCT 2001 (Ref. 40; Last annotation update)  
DE Myosin light chain kinase, smooth muscle (E027.1.117) (MOLCK)  
DE Contains: telokin.  
GN MYLK.  
OC Crystallinus, cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cytodactylus.  
OX NCBI TaxID 9986;  
FN [1]  
FE SEQUENCE FROM N.A.  
FE ISSUES: Smooth muscle.  
RX MEDLINE 92094691; PubMed 1749666;  
KA Gallagher P.J.; Herring B.P.; Griffin S.A.; Stull J.T.;  
KT "Molecular characterization of a mammalian smooth muscle myosin light  
KT chain kinase."  
KT J. Biol. Chem. 266:23936-23944 (1991).  
FN [2]  
RP SEQUENCE of 993 1147 FROM N.A. (TELOKIN).  
RX MEDLINE 92094691; PubMed 1749666;  
KA Gallagher P.J.; Herring B.P.;  
KT "The carboxyl terminal of the smooth muscle myosin light chain kinase  
KT is expressed as an independent protein, telokin."  
KT J. Biol. Chem. 266:23945-23952 (1991).

CC FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A  
CC MYOSIN LIGHT CHAIN.  
CC CATALYTIC ACTIVITY: ATP + myosin light chain -> ADP + myosin  
CC light-chain phosphate.  
CC ALTERNATIVE PHOSPHATASE. AS AACT, THERE IS EVIDENCE THAT MYLK ARE PRODUCE  
CC BY ALTERNATIVE INITIATION. A NEW MUSCLE FORM (WHICH IS THE LONGEST  
CC 15K). A chain has 11K, 12K, 14K, and 16K (A, B, C, D) TERMINAL, ALL OF WHICH  
CC NO CATALYTIC ACTIVITY).  
CC DOMAIN: TELOKIN BINDS CALMODULIN.  
CC SIMILARITY: BELONGS TO THE DEUTEROPHYLID FAMILY. TELOKIN KINASES.  
CC SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2 TYPE DOMAIN.  
CC SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN TYPE 11-LIKE DOMAIN.

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DR EMBL: M76233; AAA74093.1;  
DR EMBL: M76234; AAA41408.1;  
DR EMBL: M76181; AAA41409.1;  
DR PIR: A41675; A41675;  
DR BSSP: P56276; 11LK;  
DR InterPro: IPR000719; Pak\_kinase;  
DR InterPro: IPR000066; Iq\_MBP;  
DR InterPro: IPR000066; Iq\_MBP;  
DR InterPro: IPR000598; Iq\_c2;  
DR InterPro: IPR000600; Iq-like;  
DR InterPro: IPR002290; Ser\_thr\_kinase;  
DR Pfam: PF00047; Iq; 1;  
DR Pfam: PF00047; Iq; 2;  
DR Pfam: PF00069; PKinase; 1;  
DR Pfam: PF00001; Pak\_kinase; 1;  
DR SMART: SM00060; Iq; 1;  
DR SMART: SM00410; Iq-like; 1;  
DR SMART: SM00408; Iq\_c2; 2;  
DR SMART: SM00220; S\_TKc1; 1;  
DR PROSITE: PS00107; PROTEIN\_KINASE\_AIP; 1;  
DR PROSITE: PS00108; PROTEIN\_KINASE\_S1; 1;  
DR PROSITE: PS00117; PROTEIN\_KINASE\_PPM; 1;  
KW Transferrase; Serine/threonine protein kinase; Calmodulin-binding;  
KW AIP binding; Phosphorylation; Immunoglobulin domain; Repeat;  
KW Alternative initiation;  
FT CHAIN 1 1147 MYOSIN LIGHT CHAIN KINASE; SMOOTH MUSCLE  
FT ISOZYME;  
FT TELOKIN;  
FT INIT\_MET 993 993 FOR TELOKIN;  
FT DOMAIN 100 288 16 X 12 AA TANDEN REPEATS;  
FT REPEAT 100 111 1;  
FT REPEAT 112 123 2;  
FT REPEAT 124 132 3 (INCOMPLETE).  
FT REPEAT 133 144 4;  
FT REPEAT 145 156 5;  
FT REPEAT 157 168 6;  
FT REPEAT 169 180 7;  
FT REPEAT 181 192 8;  
FT REPEAT 193 204 9;  
FT REPEAT 205 216 10;  
FT REPEAT 217 228 11;  
FT REPEAT 229 240 12;  
FT REPEAT 241 252 13;  
FT REPEAT 253 264 14;  
FT REPEAT 265 276 15;  
FT REPEAT 277 288 16;  
FT DOMAIN 574 644 TELOKIN TYPE 111;  
FT DOMAIN 696 993 PROTEIN KINASE;  
FT DOMAIN 943 1036 CALMODULIN BINDING;  
FT DOMAIN 1036 1123 IQ-LIKE C2 TYPE DOMAIN;  
FT NT\_BIND 702 710 AIP (BY SIMILARITY);  
FT BINDING 725 725 AIP (BY SIMILARITY);



```
FT ACT_SITE 817 817 BY SIMILARITY.
FT DOMAIN 1148 1147 POLY-GLU.
FT CONFLICT 1114 1114 C -> R (IN REF. 2).
SQ SEQUENCE 1147 AA; 125719 MW; F039E624C6E31024 CRC64;

Query Match 53.2%; Score 58; DB 1; Length 1147;
Best Local Similarity 73.7%; Pred. Ref. Q.23;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0.

QY 4 PRASICTCHAVRAIGRISS 22
II II:IIIIIIIIII
Db 974 RRKWKIGNAVRAIGRISS 992

RESULT 4
KMIS_BOVIN STANDARD; PRT; 1176 AA.
AC Q29924;
DI 15-JUL-1998 (Rel. 36, Created)
DI 15-JUL-1998 (Rel. 36, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)
DE [contains: telokin].
GN MYLK.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Primates; Ruminantia; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID 9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: Stomach; PubMed:1284247;
RX MEDLINE:94293148; PubMed:1284247;
RA Kobayashi H., Iwase A., Mikawa T., Kawayama H., Hotta Y., Masaki T.,
RA Ebashi S.
RI "Isolation of cDNA for bovine stomach 155 kDa protein exhibiting
RI myosin light chain kinase activity."
RL J. Biochem. 112:786-791(1992).
CC -!- FUNCTION: CALCIUM/CALMODULIN DEPENDENT ENZYME RESPONSIBLE FOR
CC SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
CC IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC). AN EVENT THAT
CC FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS.
CC -!- CATALYTIC ACTIVITY: ATP + [myosin light chain] ADP + [myosin
CC light-chain] phosphate.
CC -!- SUBUNIT: TELOKIN BINDS CALMODULIN.
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS OF MLCK ARE PRODUCED BY
CC ALTERNATIVE INITIATION, A NON-MUSCLE FORM (WHICH IS THE LONGEST
CC FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH
CC NO CATALYTIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: S57131; AAB25794.1; -.
DR HSSP: P56276; IILK.
DR InterPro: IPR000719; Puk_pkinase
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003598; Iq_c2.
DR InterPro: IPR003600; Iq_like.
DR InterPro: IPR002990; Ser_thr_pkinase
DR Pfam: PF00041; In3; 1.
DR Pfam: PF00047; Iq; 2.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Puk_pkinase; 1.
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DR SMART: SM00060; FN3; 1.
DR SMART: SM00410; IG_Like; 1.
DR SMART: SM00408; IG2; 2.
DR SMART: SM00320; SLIC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_S1; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
FW Transferase; Serine/threonine protein kinase; Calmodulin-binding;
KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
FT CHAIN 1 1176 MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT CHAIN 1022 1176 ISUZYME.
FT INIT_MET 1022 1022 TELOKIN.
FT DOMAIN 100 291 16 X 12 AA TANDDEM REPEATS.
FT REPEAT 100 111 1.
FT REPEAT 112 123 2.
FT REPEAT 124 135 3 (INCOMPLETE).
FT REPEAT 136 147 4.
FT REPEAT 148 159 5.
FT REPEAT 160 171 6.
FT REPEAT 172 183 7.
FT REPEAT 184 195 8.
FT REPEAT 196 207 9.
FT REPEAT 208 219 10.
FT REPEAT 220 231 11.
FT REPEAT 232 243 12.
FT REPEAT 244 255 13.
FT REPEAT 256 267 14.
FT REPEAT 268 279 15.
FT REPEAT 280 291 16.
FT DOMAIN 603 673 FIBRONECTIN TYPE-III.
FT DOMAIN 725 980 PROTEIN KINASE.
FT DOMAIN 972 1035 CALMODULIN BINDING.
FT N7_BIND 731 739 10-LIKE C2-TYPE DOMAIN.
FT BINDING 754 754 ATP (BY SIMILARITY).
FT ACT_SITE 846 846 BY SIMILARITY.
FT DOMAIN 1171 1176 POLY GLU.
SQ SEQUENCE 1176 AA; 129824 MW; F53DC6D4142D4P9? CRC64;

Query Match 53.2%; Score 58; DB 1; Length 1176;
Best Local Similarity 73.7%; Pred. Ref. Q.24;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 KRASICTCHAVRAIGRISS 22
II II:IIIIIIIIII
Db 1003 RRKWKIGNAVRAIGRISS 1021

RESULT 5
KMIS_HUMAN STANDARD; PRT; 1914 AA.
AC Q15746; Q14844; Q16794; Q95796; Q95797; Q95798; Q95799; Q90865;
AC Q90IT9;
DI 15-JUL-1998 (Rel. 36, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DI 15 JUN 2002 (Rel. 41, Last annotation update)
DE Myosin light chain kinase, smooth muscle and non muscle isozymes
DE (EC 2.7.1.117) (MLCK) [negative regulation of kinase related protein]
DE (KRP)1.
GN MYLK OR MLCK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A. (Isoterm 1).
RC Tissue: epithelial cell endothelial cells;
RX MEDLINE 97304466; Pubmed 9160829;
RA Garcia J.G.N., Lazar V.L., Gilbert-Mcclain L.L., Gallagher P.J.,
RA Verin A.D.
RI "Myosin light chain kinase in endothelium: molecular cloning and
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PI regulation.";  
PI Am. J. Respir. Cell Mol. Biol. 16:489-494(1997).  
PN 121  
PP REVISIONS.  
RA Kirukov K.G., Garcia J.G.N.;  
PI Submitted (MAR 2000) to the EMBL/Genbank/DBJ databases.  
PN 131  
PP SEQUENCE FROM N.A. (ISOFORMS 2, 3A, 3B AND 4).  
PP TISSUE Embryonal zebrafish;  
PX MEDLINE 99216419; PubMed 1018165;  
RA Lazar V.J., Garcia J.G.N.;  
PI "A single human myosin light chain kinase gene (MLCK; MYLK).";  
PI Genomics 57:236-267(1999).  
PN 141  
PP REVISIONS (ISOFORM 2).  
RA Kirukov K.G., Garcia J.G.N.;  
PI Submitted (MAR 2000) to the EMBL/Genbank/DBJ databases.  
PN 151  
PP SEQUENCE OF 923-1914 FROM N.A.  
PP TISSUE Hippocampus;  
PX MEDLINE 99121667; PubMed 8976746;  
RA Potier M.C., Chelot E., Tokarsky V., Gardier E., Rossier J.,  
RA Turnell W.G.;  
PI "The human myosin light chain kinase (MLCK) from hippocampus:  
PI cloning, sequencing, expression, and localization in zebrafish";  
PI Genomics 29:552-570(1995).  
PN 161  
PP SEQUENCE OF 1414-1914 FROM N.A.  
PP TISSUE Lung, and Placenta;  
PX MEDLINE 20007840; PubMed 10566470;  
RA Waterson M.M., Schayocky J.P., Guo L., Weiss C., Chlenski A.,  
RA Shinsky V.P., Van Eldik L.J., Baloch J.;  
PI "Analysis of the kinase-related protein gene found at human chromosome  
PI 9q21 in a multi-gene cluster: organization, expression, alternative  
PI splicing and polymorphic marker";  
PI J. Cell. Biochem. 75:481-491(1999).  
PN 171  
PP SEQUENCE OF 1456-1914 FROM N.A.  
PP TISSUE Placenta;  
RA Waterson M.M.;  
PI Submitted (NOV 1995) to the EMBL/Genbank/DBJ databases.  
PP 1 FUNCTION: CALCIUM/CALMODULIN DEPENDENT ENZYME. RESPONSIBLE FOR  
PP SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE  
PP IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC). AN EVENT THAT  
PP FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS. CENTRAL  
PP DETERMINANT IN THE DEVELOPMENT OF VASCULAR PERMEABILITY AND TISSUE  
PP EDema FORMATION. IN THE NERVOUS SYSTEM IT HAS BEEN SHOWN TO  
PP CONTR. THE GROWTH INITIATION OF ASPHYCTIC PROCESSES IN CULTURE  
PP AND TO PARTICIPATE IN TRANSMITTER RELEASE AT SYNAPSES FORMED  
PP BETWEEN CULTURED SYMPATHETIC GANGLION CELLS. CRITICAL PARTICIPANT  
PP IN SIGNALING SEQUENCES THAT RESULT IN PRECOCIAL APOPTOSIS.  
PP 1 CATALYTIC ACTIVITY: ATP + [myosin light chain] -> ADP + [myosin  
PP light chain] phosphate.  
PP 1 SUBUNIT: TETRAMER. CALMODULIN.  
PP 1 ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS: 1 (SPERM HEAD), 2, 3A,  
PP 3B, 4 AND DEL 1790; ARE PRODUCED BY ALTERNATIVE SPLICING.  
PP 1 TISSUE SPECIFICITY: SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES ARE  
PP EXPRESSED IN A WIDE VARIETY OF ADULT AND FETAL TISSUES AND IN  
PP CULTURED ENDOTHELIUM WITH QUALITATIVE EXPRESSION APPEARING TO BE  
PP NEITHER TISSUE- NOR DEVELOPMENT SPECIFIC. NON-MUSCLE ISOFORM 2 IS  
PP THE DOMINANT SPLICED VARIANT EXPRESSED IN VARIOUS TISSUES. TETRAMER  
PP HAS BEEN FOUND IN A WIDE VARIETY OF ADULT AND FETAL TISSUES.  
PP 1 PIM: MLCK IS PROBABLY DOWN REGULATED BY PHOSPHORYLATION.  
PP 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
PP 1 SIMILARITY: CONTAINS 1 TETRACLOLEIN LIKE 12-TYPE DOMAIN.  
PP 1 SIMILARITY: CONTAINS 1 TETRACLOLEIN TYPE 11 LIKE DOMAIN.  
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CC  
DR EMBL: U48959; AAC18423.2;  
DR EMBL: AF069631; AAD15921.2;  
DR EMBL: AF069602; AAD15922.1;  
DR EMBL: AF069603; AAD15923.1;  
DR EMBL: AF069604; AAD15924.1;  
DR EMBL: AF5337; CAA59685.1;  
DR EMBL: AF096771; AAD51380.1;  
DR EMBL: AF096766; AAD51380.1;  
DR EMBL: AF096767; AAD51380.1;  
DR EMBL: AF096768; AAD51380.1;  
DR EMBL: AF096769; AAD51380.1;  
DR EMBL: AF096770; AAD51380.1;  
DR EMBL: AF096771; AAD51380.1;  
DR EMBL: AF096772; AAD51380.1;  
DR EMBL: AF096773; AAD51380.1;  
DR EMBL: AF096774; AAD51380.1;  
DR EMBL: AF096775; AAD51380.1;  
DR EMBL: AF096776; AAD51380.1;  
DR EMBL: AF096777; AAD51380.1;  
DR EMBL: AF096778; AAD51380.1;  
DR EMBL: AF096779; AAD51380.1;  
DR EMBL: AF096780; AAD51380.1;  
DR HSP: Q63450; IAO6.  
DR Genbank: BCN57590; MYLK.  
DR MIM: 600922;  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003961; FN\_111.  
DR InterPro: IPR003962; Full\_repeat.  
DR InterPro: IPR003096; T4\_MBO.  
DR InterPro: IPR003598; T4\_C2.  
DR InterPro: IPR003600; T4\_Like.  
DR InterPro: IPR02290; Ser\_thr\_kinase.  
DR Pfam: PF00041; t4; 1.  
DR Pfam: PF00047; t4; 8.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00014; FNYPE111.  
DR Pfam: PF00001; Euk\_pkinase; 1.  
DR SMART: SM00060; FN3; 1.  
DR SMART: SM00410; IG\_Like; 1.  
DR SMART: SM00408; IG2; 8.  
DR SMART: SM0220; S\_Like; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_AIP; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_SI; 1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
KW Transposase; Serine/threonine-protein kinase; Calmodulin binding;  
KW ATP binding; Phosphorylation; Immunoglobulin domain; Repeat;  
KW Alternative initiation; Alternative  
PP CHAIN 1 1914  
PP MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE  
PP ISOZYME.  
PP CHAIN 923 1914  
PP MYOSIN LIGHT CHAIN KINASE, SMOOTH  
PP ISOZYME.  
PP CHAIN 1761 1914  
PP TETROKIN.  
PP IN11\_MEF 923 1914  
PP FOR MYOSIN LIGHT CHAIN KINASE, SMOOTH  
PP MUSCLE ISOZYME.  
PP IN11\_MEF 1761 1914  
PP FOR TETROKIN.  
PP DOMAIN 143 1413  
PP TETROKIN TYPE 111.  
PP DOMAIN 1464 1719  
PP PROTEIN KINASE.  
PP DOMAIN 1711 1774  
PP CALMODULIN BINDING.  
PP DOMAIN 1824 1891  
PP 12 LIKE 12 TYPE DOMAIN  
PP NE\_BIND 1470 1478  
PP ATP (BY SIMILARITY)  
PP BINDING 1433 1433  
PP ATP (BY SIMILARITY).  
PP A1\_SITE 1585 1585  
PP POLY-GLU  
PP DOMAIN 1906 1914  
PP 3 X 20 AA ALTERNATE TANDem REPEATS.  
PP DOMAIN 868 895  
PP 1 1.  
PP REPEAT 896 923  
PP 1 2.  
PP REPEAT 924 951  
PP 1 3.  
PP REPEAT 952 979  
PP 1 4.  
PP REPEAT 980 998  
PP 1 5. (INCOMPLETE).  
PP DOMAIN 999 1063  
PP 6 X 12 AA APPROXIMATE TANDem REPEATS.  
PP REPEAT 999 1003  
PP 11-1 (INCOMPLETE).  
PP REPEAT 1004 1015  
PP 11-2.





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DR EMBL: Z50023; CAA90326.1; -  
DR InterPro: IPR001451; Hexapep\_transf.  
DR InterPro: IPR001825; NTP\_transferase.  
DR Pfam: PF00132; hexapop; 7.  
DR Pfam: PF00483; NTP\_transferase; 1.  
DR TIGFAMS: TIGR01173; glam; 1.  
DR PROSITE: PS00101; HEXAPEP\_TRANSFERASES; FALSE\_NEG.  
KW Transferase, Acyltransferase, Nucleotidyltransferase,  
KW Multifunctional enzyme, Peptidoglycan synthesis, Cell wall, repeat.  
SQ SEQUENCE 456 AA 48838 MW 76AF6AG7F7956666 CRC64.

Query Match 38.1% Score 41.5; DB 1; Length 456;  
Best Local Similarity 62.5%; Pred. No. 37;  
Matches 10; Conservative 3; Mismatches 2; Indels 1; Caps 1;

QY 8 LGIGHAVR-AIGRISS 22  
|||||: 1: 1:1  
DB 79 LGIGHAVKALPHLAS 94

RESULT 10  
RTCA\_METIH  
ID RTCA\_METIH STANDARD; PRT; 337 AA.  
AC 027937;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Probable RNA 3'-terminal phosphate cyclase (EC 3.1.1.4) (RNA 3'-  
DE phosphate cyclase) (RNA cyclase).  
GN RTCA OR MTH1915.  
OS Methanobacterium thermoautotrophicum.  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales,  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=187420;  
PN 111  
RP SEQUENCE FROM N.A.  
RC STRAIN Delta H;  
RX MEDLINE=98037514; PubMed=9371463;  
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,  
FA Altschuld R., Raskin J., Plak J., K. S., Hillier F.,  
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,  
RA Spadafora R., Viare P., Wang Y., Wierzbowski J., Gibson R.,  
RA Jiwan N., Caruso A., Rush D., Safer H., Patwell P., Prabhakar S.,  
RA McQuall S., Shiner G., Joyal A., Pietrovski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;  
RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
RT deltaH: functional analysis and comparative genomics."  
RL J. Bacteriol. 179:7135-7155(1997)

CC -1- FUNCTION: Catalyzes the conversion of 3' phosphate to a 2',3'-  
CC cyclic phosphodiester at the end of RNA. The mechanism of action  
CC of the enzyme occurs in 3 steps: (A) adenylation of the enzyme by  
CC ATP; (B) the enzyme acts on RNA-N3'P to produce RNA-N3'PP5'A; (C)  
CC a non-catalytic nucleophilic attack by the adjacent 2'-hydroxyl on  
CC the phosphorus in the diester linkage to produce the cyclic end  
CC product. The biological role of this enzyme is unknown but it is  
CC likely to function in some aspects of cellular RNA processing (by  
CC similarity).  
CC -1- CATALYTIC ACTIVITY: ATP + RNA 3'-terminal-phosphate + AMP +  
CC diphosphate + RNA terminal-2',3'-cyclic phosphate.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).  
CC -1- SIMILARITY: BELONGS TO THE RNA 3'-TERMINAL CYCLASE FAMILY.  
CC SUBFAMILY 1.

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DR EMBL: AF000942; AAB86375.1; -  
DR HSP: P46849; IQMH.  
DR InterPro: IPR000228; RNA3'\_term\_cycl.  
DR Pfam: PF01137; RTC; 1.  
DR PROSITE: PS01287; RTC; 1.  
KW Ligase; Complete proteome.  
FT ACT\_SITE 306 306 BY SIMILARITY.  
SQ SEQUENCE 337 AA 35922 MW 98934669743PP CRC64;

Query Match 37.6% Score 41; DB 1; Length 337;  
Best Local Similarity 43.5%; Pred. No. 32;  
Matches 10; Conservative 4; Mismatches 5; Indels 4; Gaps 1;

QY 4 PRASLCTCH---AVRAIGRISS 22  
|||||: 1: 1:1:1:1:1:1:  
DB 38 PRASLCTCHGHLIAVAVAVAEISN 60

RESULT 11  
CPR6\_CAREL  
ID CPR6\_CAREL STANDARD; PRT; 379 AA.  
AC P43510;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cathepsin B-like cysteine proteinase 6 precursor (EC 3.4.22.-)  
DE (Cysteine protease related 6).  
GN CPR-6 OR C25B8.3.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Eubiotitida; Platyhelminthes;  
OC Rhabditidae; Peloderidae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN 111  
RP SEQUENCE FROM N.A.  
RC STRAIN Bristol N2;  
RA Larmann C.G.C., Johnstone I.L.;  
EL Submitted (MAY-1995) to the EMBL/GenBank/Tran databases.  
RN 121  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
RA Waterston R.;  
EL Submitted (MAY-1995) to the EMBL/GenBank/Tran databases.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
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DR EMBL: L39894; AAA98787.1; -  
DR EMBL: L39893; AAA98789.1; -  
DR EMBL: P41550; AAA39189.1; -  
DR HSP: P07688; IQDQ.  
DR MEROPS: C01.0PA; -  
DR WormPop: C25B8.3; CE04078.  
DR InterPro: IPR000668; Peptidase\_C1.  
DR InterPro: IPR000166; Supra\_site.  
DR Pfam: PF00112; Peptidase\_C1; 1.  
DR PRINTS: PR00705; PAPAIN.  
DR ProDom: PD000158; Peptidase\_C1; 1.  
DR PROSITE: PS00139; THIOL\_PROTEASE\_CYS; 1.  
DR PROSITE: PS00639; THIOL\_PROTEASE\_HIS; 1.  
DR PROSITE: PS00640; THIOL\_PROTEASE\_ASN; 1.  
KW Hydrolase, Thiol protease, Symmetric Signal.  
FT SIGNAL 1 16 POTENTIAL.

FI PROPEP 17 134 POTENTIAL.  
 FI CHAIN 379 379 CATHESPIN B LIKE CYSTEINE PROTEINASE 6.  
 FI A\*1 SITE 133 133 BY SIMILARITY.  
 FI A\*1 SITE 325 325 BY SIMILARITY.  
 FI A\*1 SITE 325 325 BY SIMILARITY.  
 FI DISULFID 138 138 BY SIMILARITY.  
 FI DISULFID 130 134 BY SIMILARITY.  
 FI DISULFID 166 233 BY SIMILARITY.  
 FI DISULFID 167 170 BY SIMILARITY.  
 FI DISULFID 203 247 BY SIMILARITY.  
 FI DISULFID 211 223 BY SIMILARITY.  
 FI CARBOHYD 196 196 N LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 379 AA: 42404 MW: 4087369061925F CR6647  
 Query Match 37.6% Score 41: DB 1: Length 379;  
 Best Local Similarity 72.7% Pred. No. 37;  
 Matches 8: Conservative 1: Mismatches 2: Indels 0: Gaps 0.  
 27 R LHHSHAVRAVG 18  
 11 11111111  
 DB 301 LHHSHAVRAVG 311  
 RESULT 12  
 ALGX PPTAN STANDARD: PRT: 664 AA.  
 A\* 604841;  
 D1 13 AUG 1987 (Rev. 05, Created)  
 D1 13 AUG 1987 (Rev. 05, Last sequence update)  
 D1 01 NOV 1997 (Rev. 35, Last annotation update)  
 D1 Alcohol oxidase (EC 1.1.3.13) (A\*1) (Molecular oxidase) (M-X).  
 GN Mox.  
 OS Pichia angusta (Yeast) (Hansenula polymorpha).  
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OS Saccharomycetales; Saccharomycetaceae; Pichia.  
 OS Nqaf 1 (X) 405;  
 GN 111  
 FP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 FX MEDLINE 85215671: PubMed 2582370;  
 RA Leclercq A.M., Edema J., Mar J., Vinger J., Verrips C.F.,  
 R1 "Molecular cloning and characterization of a gene coding for methanol  
 R1 oxidase in Hansenula polymorpha."  
 R1 Nucleic Acids Res. 13:3063-3082(1985)  
 R1 121  
 R1 SIMILARITY TO LHHSHAVRAVG: 664 AA.  
 R1 MEDLINE 9110223: PubMed 2582370;  
 RA Carver J.P., Krassov P.  
 R1 "Hansenula glucose dehydrogenase and yeast alcohol oxidase are  
 R1 homologous and share N-terminal homology with other flavoenzymes."  
 R1 Mol. Biol. Evol. 8:144-150(1991).  
 R1 131  
 R1 REVIEW.  
 R1 MEDLINE 9110274: PubMed 1882546;  
 RA van der Klei J.J., Harder W., Veenhuis M.  
 R1 "Biosynthesis and assembly of alcohol oxidase, a peroxisomal matrix  
 R1 protein in methylotrophic yeasts: a review."  
 R1 Yeast 7:195-209(1991).  
 R1 1 CATALYTIC ACTIVITY: A primary alcohol + O(2) -> an aldehyde +  
 R1 H(2)O(2).  
 R1 1 COFACTOR: FAD.  
 R1 1 PATHWAY: 11 IS THE FIRST REACTION IN 11 METABOLISM IN YEAST  
 R1 WHEREIN METHANOL IS OXIDIZED TO FORMALDEHYDE, WHICH IS THEN  
 R1 BROKEN DOWN TO CARBON DIOXIDE.  
 R1 1 SUBUNIT: HOMODIMER.  
 R1 1 SUBCELLULAR LOCATION: Peroxisomal.  
 R1 1 SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.  
 R1  
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 CC  
 DR EMBL: X02425; CAA26278.1;  
 DR EMBL: A11156; CAA00941.1;  
 DR EMBL: A23010; OXHAAP;  
 DR InterPro: IPR000172; GMC\_oxid.  
 DR Pfam: PF00732; GMC\_oxid; 1.  
 DR PROSITE: PS00342; MICROBODIES\_CTER; 1.  
 DR PROSITE: PS00623; GMC\_OXRED\_1; 1.  
 DR PROSITE: PS00624; GMC\_OXRED\_2; 1.  
 KW oxidoreductase; Flavoprotein; FAD; Methanol utilization; Peroxisome.  
 FI NP\_BIND 8 59 FAD (AUX PART) (POTENTIAL).  
 FI ACT\_SITE 573 574 MICROBODIES\_CTER647.  
 FI SITE 662 664  
 FI SEQUENCE 664 AA: 74089 MW: 6463476688050 CR6647  
 Query Match 37.6% Score 41: DB 1: Length 664;  
 Best Local Similarity 37.5% Pred. No. 66;  
 Matches 6: Conservative 6: Mismatches 4: Indels 0: Gaps 0.  
 QY 3 LRRKASTATGHAVRATG 18  
 1111111111111111  
 DB 278 LRRKASTATGHAVRATG 293  
 RESULT 13  
 PMAI CANAL  
 D1 PMAI CANAL STANDARD: PRT: 895 AA.  
 AC 128877;  
 D1 01 DEC 1992 (Rev. 24, Created)  
 D1 01 DEC 1992 (Rev. 24, Last sequence update)  
 D1 16 OCT 2001 (Rev. 40, Last annotation update)  
 DE Plasma membrane ATPase 1 (EC 3.6.3.6) (Proton pump 1).  
 GN PMAI  
 OS Candida albicans (Yeast).  
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OS Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OS Nqaf 1 (X) 5476;  
 GN 111  
 FP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE 92041566: PubMed 1834633;  
 RA Monk B.C., Kurtz M.R., Martinian J.A., Perlman D.S.  
 R1 "Cloning and characterization of the plasma membrane H(+) ATPase from  
 R1 Candida albicans."  
 R1 J. Bacteriol. 173:6826-6836(1991).  
 R1 1 FULL-OR: THE PLASMA MEMBRANE ATPASE OF CANDIDA ALBICANS IS A  
 R1 HYDROGEN ION PUMP. THE GENE CODING IT GENERATES DRIVES THE  
 R1 ACTIVE TRANSPORT OF NUTRIENTS BY H+ SYMPORT. THE RESULTING  
 R1 EXTERNAL ACIDIFICATION FOR A 2% INTERNAL ALKALIZATION MAY MEDULATE  
 R1 GROWTH RESPONSES.  
 R1 1 CATALYTIC ACTIVITY: ATP + H(2)O -> H(+) (in) ADP + phosphate +  
 R1 H(+) (out).  
 R1 1 SUBCELLULAR LOCATION: Integral membrane protein.  
 R1 1 SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY  
 R1 (E1-E2 ATPASES). SUBFAMILY 111A.  
 R1  
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 R1 or send an email to license@ebi.ac.uk.  
 R1  
 R1 EMBL: M74075; AAA43419.1;  
 DR PIR: A41336; PXCKP.  
 DR InterPro: IPR001757; ATPase\_E1\_E2.  
 DR InterPro: IPR004014; Cation\_ATPase.  
 DR InterPro: IPR000695; H\_ATPase.  
 DR InterPro: IPR001454; Hydase/hydrolase.  
 DR Pfam: PF00122; E1-E2\_ATPase; 1.  
 DR Pfam: PF00690; Cation\_ATPase\_N; 1.  
 DR Pfam: PF00732; Hydrolase; 1.



DR PRINTS: PRO0119; CATAIPASE.  
DR PRINTS: PRO0120; HAIPASE.  
DR PROSITE: PS00154; AIPASE\_E1\_E2; 1.  
KW Hydrolyse, hydrolytic, Transports, Transmembrane, Phosphorylation.  
KW Magnesium; ATP-binding; Multigene family.  
FT DOMAIN 1 92 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 93 113 1 (POTENTIAL).  
FT DOMAIN 114 117 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 118 137 2 (POTENTIAL).  
FT DOMAIN 138 268 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 269 290 3 (POTENTIAL).  
FT DOMAIN 291 301 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 302 324 4 (POTENTIAL).  
FT DOMAIN 325 696 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 697 715 5 (POTENTIAL).  
FT DOMAIN 716 731 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 732 751 6 (POTENTIAL).  
FT DOMAIN 752 801 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 802 822 7 (POTENTIAL).  
FT DOMAIN 823 924 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 835 851 8 (POTENTIAL).  
FT DOMAIN 852 895 CYTOPLASMIC (POTENTIAL).  
FT MOD\_RES 896 955 PROSERIFICATION (PY SIMILARITY).  
FT METAL 611 611 MAGNESIUM (BY SIMILARITY).  
FT METAL 615 615 MAGNESIUM (PY SIMILARITY).  
SQ SEQUENCE 995 AA; 97459 MW; 20F2451BD3CB25B1 CRC64;

Query Match 37.6%; Score 41; DB 1; Length 895;  
Best Local Similarity 33.3%; Prod. No. 91;  
Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0.

QY 3 LRRASLGTHAVRAIGRLST 23  
DB 253 VNFAASNGHPTFVNLCTT 272

RESULT 14  
ID ALAL\_CANAL STANDARD; PRI: 1419 AA.  
AC Q23468;  
DI 15-JUL-1999 (Rel. 38, Created)  
DI 15-JUL-1999 (Rel. 38, Last sequence update)  
DI 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Agglutinin-like protein ALAL precursor (Agglutinin-like adhesion).  
GN ALAL OR ALS.  
OS Candida albicans (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.  
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5476;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98053977; PubMed=9293828;  
PA Cit. N.Y. 1997; 5 A.1.  
RI "Expression, cloning, and characterization of a Candida albicans  
RI gene, ALAL, that confers adherence properties upon Saccharomycetes  
RI cerevisiae for extracellular matrix proteins.";  
RL Infect. Immun. 65:5289-5294(1997).  
CC -!- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.  
CC -!- PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED (POTENTIAL).  
CC -----  
CC This SWISS PROT entry is copyrighted. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
DR EMBL: AF025429; AAB88883.1; .  
KW Cell adhesion, glycoprotein, Repeat, Signal  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 1419 AGGLUTININ LIKE PROTEIN ALAL.  
FT DOMAIN 199 404 POLY-THR.

FT DOMAIN 408 418 POLY-THR.  
FT DOMAIN 437 441 POLY-THR.  
FT DOMAIN 673 676 POLY-SER.  
FT DOMAIN 687 690 POLY-SER.  
FT DOMAIN 700 703 POLY-SER.  
FT DOMAIN 719 724 POLY-SER.  
FT DOMAIN 749 752 POLY-SER.  
FT DOMAIN 787 791 POLY-SER.  
FT DOMAIN 869 872 POLY-SER.  
FT DOMAIN 875 883 POLY-SER.  
FT DOMAIN 901 911 POLY-SER.  
FT DOMAIN 1216 1221 POLY-SER.  
FT CARBOHYD 665 665 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 919 919 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 1301 1301 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 1326 1326 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 1419 AA; 14065 MW; 219F337C99A9566 CRC64;

Query Match 37.6%; Score 41; DB 1; Length 1419;  
Best Local Similarity 40.9%; Prod. No. 155-02;  
Matches 9; Conservative 3; Mismatches 10; Indels 0; Gaps 0.

QY 1 TELEFASLGTHAVRAIGRLST 22  
DB 1212 TELESTSSGNHATLGGSTVKS 1293

RESULT 15  
ID A10C\_HUMAN STANDARD; PRI: 1499 AA.  
AC Q60312; Q96914;  
DI 30 MAY 2000 (Rel. 39, Created)  
DI 15-JUN 2002 (Rel. 41, Last sequence update)  
DI 15-JUN 2002 (Rel. 41, Last annotation update)  
DE Potential phospholipid-transporting ATPase VC (EC 3.6.3.1) (AIPVC).  
DE (Aminophospholipid translocase VC).  
GN ATP10C OR AIPVC OR KIAA0566.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21225279; PubMed 11326269;  
PA Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.,  
RA Oshimura M.;  
RI "A novel naturally expressed gene, ATP10C, encodes a putative  
RI aminophospholipid translocase associated with Angelman syndrome.";  
RL Nat. Genet. 28:19-20(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21313119; PubMed=11353404;  
PA Herzig L.B.K., Kim S.-I., Cook E.H. Jr., Ledbetter D.H.;  
RI "The human aminophospholipid transporting ATPase gene ATP10C maps  
RI adjacent to URB3A and exhibits similar imprinted expression.";  
RL Am. J. Hum. Genet. 68:1501-1505(2001).  
RN [3]  
RP SEQUENCE OF 337 1499 FROM N.A.  
RX TISSUE=Brain;  
RX MEDLINE=98290545; PubMed=9628581;  
RA Kase H., Ishikawa K. I., Matsujima N., Tanaka A., Kotani H.,  
RA Nomura N., Ohara O.;  
RI "Prediction of the coding sequences of unidentified human genes. IX.  
RI The complete sequences of 100 new cDNA clones from brain which can  
RI code for large proteins in vitro.";  
RL LNA E. 7: 37-36(1998).  
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O ADP + phosphate.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
CC -!- TISSUE SPECIFICITY: Wide expression, with higher levels in  
CC kidney, followed by lung, brain, prostate, testis, ovary, and  
CC small intestine.  
CC -!- DISEASE: Defects in ATP10C may be a cause of Angelman syndrome  
CC (AS), also known as 'happy puppet syndrome'.

1 SIMILARITY: BELONGS TO THE CALIUM TRANSPORT ATPASES FAMILY (E1 E2  
2 ATPASES), SUBFAMILY IV.  
3  
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9 entities requires a license agreement (Go to <http://www.ebi.ac.uk/seqdb/doc/>  
10 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

11 EMBL: AB051358; BAB47392.1;  
12 EMBL: AY029594; AAK33100.1;  
13 EMBL: AY029437; AAK33100.1; JOINED.  
14 EMBL: AY029486; AAK33100.1; JOINED.  
15 EMBL: AY029489; AAK33100.1; JOINED.  
16 EMBL: AY029499; AAK33100.1; JOINED.  
17 EMBL: AY029491; AAK33100.1; JOINED.  
18 EMBL: AY029492; AAK33100.1; JOINED.  
19 EMBL: AY029493; AAK33100.1; JOINED.  
20 EMBL: AY029494; AAK33100.1; JOINED.  
21 EMBL: AY029495; AAK33100.1; JOINED.  
22 EMBL: AY029496; AAK33100.1; JOINED.  
23 EMBL: AY029497; AAK33100.1; JOINED.  
24 EMBL: AY029498; AAK33100.1; JOINED.  
25 EMBL: AY029499; AAK33100.1; JOINED.  
26 EMBL: AY029500; AAK33100.1; JOINED.  
27 EMBL: AY029501; AAK33100.1; JOINED.  
28 EMBL: AY029502; AAK33100.1; JOINED.  
29 EMBL: AY029503; AAK33100.1; JOINED.  
30 EMBL: AB011138; BAA25492.1;  
31 Genes: HBB:1547; ATP10c.  
32 MIM: 605855;  
33 MIM: 105830;  
34 InterPro: IPR001757; ATPase E1 E2.  
35 InterPro: IPR001454; Rhinase/hydrolase.  
36 Pfam: PF00702; Hydrolase\_1.  
37 Pfam15: pf00119; CATALPASE.  
38 ProSite: PS00154; ATPase E1 E2; 1.  
39 Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP binding;  
40 Multitopology.  
41 Domain 1 86 CYTOPLASMIC (POTENTIAL).  
42 TRANSMEM 67 106 POTENTIAL.  
43 Domain 107 110 EXTRACELLULAR (POTENTIAL).  
44 TRANSMEM 111 128 POTENTIAL.  
45 Domain 129 399 CYTOPLASMIC (POTENTIAL).  
46 TRANSMEM 310 352 POTENTIAL.  
47 Domain 337 362 EXTRACELLULAR (POTENTIAL).  
48 TRANSMEM 363 384 POTENTIAL.  
49 Domain 385 1087 CYTOPLASMIC (POTENTIAL).  
50 TRANSMEM 1088 1198 POTENTIAL.  
51 Domain 1199 1119 EXTRACELLULAR (POTENTIAL).  
52 TRANSMEM 1120 1140 POTENTIAL.  
53 Domain 1141 1170 CYTOPLASMIC (POTENTIAL).  
54 TRANSMEM 1171 1192 POTENTIAL.  
55 Domain 1193 1199 EXTRACELLULAR (POTENTIAL).  
56 TRANSMEM 1200 1222 POTENTIAL.  
57 Domain 1223 1228 CYTOPLASMIC (POTENTIAL).  
58 TRANSMEM 1229 1249 POTENTIAL.  
59 Domain 1250 1267 EXTRACELLULAR (POTENTIAL).  
60 TRANSMEM 1268 1292 POTENTIAL.  
61 Domain 1293 1499 CYTOPLASMIC (POTENTIAL).  
62 Mod\_RES 427 427 PHOSPHORYLATION (BY SIMILARITY).  
63 METAL 1031 1031 MAGNESIUM (BY SIMILARITY).  
64 METAL 1035 1035 MAGNESIUM (BY SIMILARITY).  
65 Domain 467 470 POLY GLU.  
66 CONFLICT 388 388 Q - R (IN REF. 3).  
67 SEQUENCE 1499 AA; 167687 MW; 14996A4D0635A68b CRC64;

Query Match 37.6% Score 41; DB 1; Length 1499;  
Best local Similarity 40.06; Pred. No. 1,6002;  
Matches 8; Conservat 100 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 KRASLGTHAVPAIGRLNSI 23  
||| 111 111 111  
DB 480 QROSLGSHQSVRVVVRKQSI 499  
  
Search completed: January 2, 2003, 12:26:58  
Job time: 7 secs





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M protein protein search, using sw model

Run on: January 2, 2003, 12:26:32 ; Search time 24.5 Seconds  
(without alignment)  
193,432 hits; 611 updated/score

Title: US 09 786 317-2  
Perfect score: 109  
Sequence: 1 LSTKRASLGLGHAVRAIGRLSSI 23

Scoring table: BLAST06.2  
Gapop 10.0 ; Gapext 0.5

Searched: 671580 seqs, 299347115 residues 671580  
Total number of hits satisfying chosen parameters:

Minimum hit seq length: 0  
Maximum hit seq length: 200000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database: SPTREMBL 21:\*
- 1: sp archaea:\*
  - 2: sp bacteria:\*
  - 3: sp fungi:\*
  - 4: sp human:\*
  - 5: sp invertebrate:\*
  - 6: sp mammal:\*
  - 7: sp mhc:\*
  - 8: sp orquanelle:\*
  - 9: sp phage:\*
  - 10: sp plant:\*
  - 11: sp rodent:\*
  - 12: sp virus:\*
  - 13: sp vertebrate:\*
  - 14: sp unclassified:\*
  - 15: sp virus:\*
  - 16: sp bacteriophage:\*
  - 17: sp archaea:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	66	60.6	907	13	Q98850	carassius a
2	58	53.2	641	6	Q98869	macaca fasc
3	58	53.2	992	4	Q96015	homo sapien
4	52	47.7	1201	2	Q9X0H8	leioneleia
5	49	45.0	237	17	Q97VX4	sulfolobus
6	49	45.0	623	5	Q96VR0	drosofila
7	49	45.0	732	5	Q961V1	drosofila
8	49	45.0	786	5	Q96V79	drosofila
9	49	45.0	832	5	Q96V53	drosofila
10	49	45.0	913	5	Q9V7G6	drosofila
11	49	45.0	929	5	Q96V51	drosofila
12	48	44.0	541	5	Q9WQ27	leishmania
13	48	44.0	615	5	Q9N9G6	leishmania
14	47	43.1	133	5	Q18906	caenorhabdi
15	47	43.1	597	16	Q9F9R3	xytella fab
16	47	43.1	1745	3	Q961X5	carassius a

17	47	43.1	2294	5	Q9N3X8	caenorhabdi
18	46.5	42.7	361	2	Q9X0Y2	rhodospirill
19	46	42.2	299	15	Q79150	human immun
20	46	42.2	454	16	Q8XH13	elostridium
21	46	42.2	456	16	Q97E92	elostridium
22	46	42.2	714	2	Q92H31	rhodospirill
23	45	41.3	96	12	Q05399	human astro
24	45	41.3	143	16	Q9R098	vibrio chol
25	45	41.3	217	16	Q9JN78	streptomyces
26	45	41.3	232	17	Q9V237	pyrococcus
27	45	41.3	360	17	Q9X0Y9	aeropyrum p
28	45	41.3	457	16	Q9HXF8	pseudomonas
29	45	41.3	787	12	Q82452	human astro
30	44.5	40.8	212	17	Q82YH3	pyrobaculum
31	44	40.4	254	15	188357	human immun
32	44	40.4	434	16	Q98039	rhizobium l
33	44	40.4	452	16	Q9S216	streptomyces
34	44	40.4	458	17	Q95947	sulfolobus
35	44	40.4	538	16	Q9K217	dictyococcus
36	43.5	39.9	336	16	Q9RDM2	streptomyces
37	43	39.4	233	17	Q9HR96	halobacteri
38	43	39.4	315	16	Q8Y0K3	bruceella m
39	43	39.4	338	16	Q9PA14	xytella fab
40	43	39.4	456	16	Q55504	synochocyst
41	43	39.4	477	16	Q9HY92	pseudomonas
42	43	39.4	533	2	Q9Z9N5	bacillus ba
43	43	39.4	534	16	Q9K154	bacillus ba
44	43	39.4	618	10	Q91W05	oryza sativ
45	43	39.4	968	16	Q33296	mycobacteri

ALIGNMENTS

RESULT 1

Q98850	PRELIMINARY;	PR1	907 AA.
ID Q98850			
AC Q98850			
DI 01-FEB-1997 (Trembl et al. 02, Created)			
DI 01-FEB-1997 (Trembl et al. 02, Last sequence update)			
DI 01-MAR-2002 (Trembl et al. 20, Last annotation update)			
DE Neuronal myosin light chain kinase 1.			
GN GPMCK1.			
OS Carassius auratus (Goldfish).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC Cyprinidae; Carassius.			
OX NCBI_TaxId 7957;			
RN 111			
RP SEQUENCE FROM N.A.			
RC STRAIN COMMON COMET;			
RX MEDLINE:97067382; PubMed 8910795;			
RA Jian X., Szabo H.G., Schmidt J.L.;			
RT "Myosin light chain kinase: expression in neurons and upregulation during axon regeneration."			
RI J. Neurobiol. 31:379-391(1996).			
CC 1 SIMILARITY: BELONG TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR EMBL: U61731; AAB41402.1;			
DR BSSP: P56276; 111K.			
DR InterPro: IPR000719; Euk_pkinase.			
DR InterPro: IPR003961; FN_111.			
DR InterPro: IPR003598; Iq_22.			
DR InterPro: IPR003006; Iq_MHC.			
DR InterPro: IPR002290; Ser_thr_kinase.			
DR Pfam: PF00041; Iq3; 1.			
DR Pfam: PF00047; Iq; 2.			
DR Pfam: PF00069; pkinase; 1.			
DR ProDom: PD000001; Euk_pkinase; 1.			
DR SMART: SM00060; FN3; 1.			
DR SMART: SM00408; Iq2; 2.			
DR SMART: SM00220; S_LTRK; 1.			
DR PROSITE: PS0107; PROTEIN KINASE A/D; UNKNOWN 1.			
DR PROSITE: PS0011; PROTEIN KINASE LHM; 1.			



EMBL: AF552704; AAL41562.1;  
InterPro: IPR014497; IPR;  
SEQUENCE 1201 AA; 134365 MW; 564ABEE5F3526D04 CPO64;

Query Match 47.7%; Score 52; DB 2; Length 1201;  
Best Local Similarity 55.0%; Pred. No. 18;  
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Q7 4 PRASINCHAVRAIGRLESS; 23  
3 111 111 111  
997 KAASGNGNAYALGISEI 1016

RESULT 6  
Q9/VX4 PRELIMINARY; PRI: 237 AA;  
Q9/VX4;

01 01 2001 (1REMBLrel. 16; Created)  
01 01 2001 (1REMBLrel. 18; Last sequence update)  
01 01 2001 (1REMBLrel. 18; Last annotation update)  
1E Serine phosphatase nucleotidyl transferase (EC 2.7.7.1).  
S502479.

Sulfolobus solfataricus.  
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
Sulfolobus.  
NCBI TaxID 2287;

SEQUENCE FROM N.A.  
STRAIN A100 35092 / DSM 1617 / P2;  
MEDLINE 2332266; PubMed 1142726;  
Shu Q., Smith P.K., Contafioneri F., Zivanovic Y., Aillard G.,  
Awaryz M., Chan-Wisher C.C., Yoo J., Clausen T.G., Curtis B.A.,  
De Meats A., Krause G., Fletcher G., Gordon P.M.K.,  
Holkamp de Jong T., Jeffrey A.C., Kozera C.J., Medina N., Pond X.,  
Thi Ngoc H.P., Redder P., Schenk M.K., Thirault C., Tolstrup N.,  
Charlebois R.L., Doolittle W.F., Inoué M., Gaasterland T.,  
Garsell P.A., Ragan M.A., Sorenson G.W., Van der West J.,  
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";  
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).

InterPro: IPR001825; NIP transferase.  
Pfam: PF00483; NIP transferase 1.  
Transferase; Nucleotidyl transferase; Complete proteome.  
SEQUENCE 237 AA; 27489 MW; 2A7A7AGDEE2933 CPO64.

Query Match 45.0%; Score 49; DB 17; Length 237;  
Best Local Similarity 50.0%; Pred. No. 9.4;  
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Q7 2 SLPRASIGCHAVRAIGRLESS; 23  
3 111 111 111  
91 SLPRFSGTVALREVEREISE 102

RESULT 6  
Q9/VX80 PRELIMINARY; PRI: 623 AA;  
Q9/VX80;

01 01 MAR 2001 (1REMBLrel. 16; Created)  
01 01 MAR 2001 (1REMBLrel. 16; Last sequence update)  
01 01 MAR 2002 (1REMBLrel. 20; Last annotation update)  
1E Stretchin-MiCK (Fracton).

STRN MiCK OR A(225) OR C68304 OR C618255.  
Drosophila melanogaster (Fruit fly).  
Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Muscomorpha;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Ephydroidea; Drosophilidae; Drosophila.  
NCBI TaxID 7227;

SEQUENCE FROM N.A.  
MEDLINE 9721868; PubMed 9147992;  
Lohtong R., Rodriguez J., Maubon D., Simcox A.,  
"Analysis of cDNAs encoding drosophila melanogaster myosin light chain

kinase.";  
J. Muscle Res. Cell Motil. 18:43-56 (1997).  
121

SEQUENCE FROM N.A.  
MEDLINE 20351481; PubMed 10991286;  
Champagne M.B., Edwards K.A., Eriksson H.P., Kiehart D.P.,  
"Drosophila stretchin-MiCK is a novel member of the titin/myosin light

chain kinase family.";  
J. Mol. Biol. 300:759-777 (2000).  
OC 1. SMILAKITY; BEL04653; THE SEK/TBK FAMILY OF PROTEIN KINASES.

EMBL: AF255669; AAG01796.1;  
HSSP: Q63450; 1A06.

FlyBase; FB00013988; Strn MiCK.  
InterPro: IPR000719; Euk\_pkinase.  
InterPro: IPR002290; Ser\_thr\_pkinase.

InterPro: IPR001245; Tyr\_pkinase.  
Pfam: PF00069; pkinase; 1.  
Pfam: PF000001; Euk\_pkinase; 1.  
SMART: SM00220; S\_TKc; 1.  
SMART: SM00219; TyrKc; 1.

PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
PROSITE: PS00198; PROTEIN\_KINASE\_ST; 1.  
KW Serine/threonine protein kinase.  
NON\_TER 1  
SEQUENCE 623 AA; 68620 MW; 792F3A76C84E0B1F CPO64;

Query Match 45.0%; Score 49; DB 5; Length 623;  
Best Local Similarity 45.0%; Pred. No. 26;  
Matches 9; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 LRRASLCHAVRAIGRLESS 22  
3 111 111 111 111  
267 LRRKWKIGNAIKALGRMAN 286

RESULT 7  
Q9GIV1 PRELIMINARY; PRI: 752 AA;  
Q9GIV1;

01 01-MAR-2001 (1REMBLrel. 16; Created)  
01 01-MAR-2001 (1REMBLrel. 16; Last sequence update)  
01 01-JUN-2002 (1REMBLrel. 21; Last annotation update)  
1E Stretchin-MiCK.

STRN MiCK OR A(225) OR C68304 OR C618255.  
Drosophila melanogaster (Fruit fly).  
Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Muscomorpha;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Ephydroidea; Drosophilidae; Drosophila.  
NCBI TaxID 7227;

SEQUENCE FROM N.A.  
MEDLINE 9721868; PubMed 9147992;  
Lohtong R., Rodriguez J., Maubon D., Simcox A.,  
"Analysis of cDNAs encoding drosophila melanogaster myosin light chain

kinase.";  
J. Muscle Res. Cell Motil. 18:43-56 (1997).  
121

SEQUENCE FROM N.A.  
MEDLINE 20351481; PubMed 10991286;  
Champagne M.B., Edwards K.A., Eriksson H.P., Kiehart D.P.,  
"Drosophila stretchin-MiCK is a novel member of the titin/myosin light

chain kinase family.";  
J. Mol. Biol. 300:759-777 (2000).  
OC 1. SMILAKITY; BEL04653; THE SEK/TBK FAMILY OF PROTEIN KINASES.

EMBL: AF255671; AAG01798.1;  
HSSP: Q63450; 1A06.

FlyBase; FB00013988; Strn MiCK.  
InterPro: IPR000719; Euk\_pkinase.  
InterPro: IPR005961; FN 111.  
InterPro: IPR002290; Ser\_thr\_pkinase.

InterPro: IPR001245; Tyr\_pkinase.  
Pfam: PF00041; 1b3; 1.  
Pfam: PF00069; pkinase; 1.  
Pfam: PF000001; Euk\_pkinase; 1.

IR SMART: SM00060; FN3; 1.  
IR SMART: SM00220; S\_TKC; 1.  
IR SMART: SM00219; TyrKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_AIP; UNKNOWN\_1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW AIP-binding; Transferase.  
SQ SEQUENCE 732 AA; 80617 MW; 72F717D1E1744AF CRC64;

Query Match 45.0%; Score 49; DB 5; Length 732;  
Best Local Similarity 45.0%; Pred. No. 31;  
Matches 9; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 LRRASLGTCHAVRAIGRLSS 22  
||| |||||  
DB 429 IRRKWKTKGNATRALGRMAN 448

RESULT 8  
Q9V7G6 PRELIMINARY; PRT: 786 AA.  
ID Q9V7G6  
AC Q9V7G6;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Stretchin-MiCK (Fragment).  
GN STPN-MiCK OR A(225) OR C08304 OR C018255.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta.  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97218368; PubMed 9147992;  
RA Lohtong K., Rodriguez D., Maughan D., Simcox A.;  
KT "Analysis of cDNAs encoding Drosophila melanogaster myosin light chain  
kinase.";  
KL J. Muscle Res. Cell Motil 18:43-56(1997).  
KN [2]  
PP SEQUENCE FROM N.A.  
RX MEDLINE=9351481; PubMed 10991286,  
RA Champagne M.B., Edwards K.A., Erickson H.P., Khabazian K.P.,  
KT "Drosophila stretchin MiCK is a novel member of the striated muscle light  
chain kinase family.";  
KL J. Mol. Biol. 300:759-777(2000).  
DR EMBL: AF255670; AAG01797.1; -.  
DR HSSP: Q63450; 1A06.  
DR FlyBase: FR00013988; Strn-MiCK.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00041; fn3; 1.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00060; FN3; 1.  
DR SMART: SM00409; IG; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_AIP; UNKNOWN\_1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 786 AA; 86163 MW; F0E1292EA03AB259 CRC64;

Query Match 45.0%; Score 49; DB 5; Length 786;  
Best Local Similarity 45.0%; Pred. No. 34;  
Matches 9; Conservative 7; Mismatches 4; Indels 1; Gaps 0;

QY 3 LRRASLGTCHAVRAIGRLSS 22  
||| |||||  
DB 440 IRRKWKTKGNATRALGRMAN 449

RESULT 9  
001653 PRELIMINARY; PRT: 832 AA.  
ID Q01653  
AC Q01653;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DI 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Myosin light chain kinase isoform-II (Fragment).  
GN STPN-MiCK OR C08304 OR C018255.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=OREGONR;  
RX MEDLINE=97223451; PubMed 9077439;  
RA Kajima S., Mishima M., Maheshi I., Hotta Y.;  
KT "A single Drosophila melanogaster myosin light chain kinase gene  
produces multiple isoforms whose activities are differently  
regulated.";  
RC Genes Cells 1:855-871(1996).  
CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR FMBL: D89663; BAA20906.1; -.  
DR HSSP: Q63450; 1A06.  
DR FlyBase: FR00013989; Strn-MiCK.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003599; Iq.  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00041; fn3; 1.  
DR Pfam: PF00047; iq; 1.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00060; FN3; 1.  
DR SMART: SM00409; IG; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_AIP; UNKNOWN\_1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Alternative splicing; Myosin; Serine/threonine-protein kinase.  
FT NON\_TER 1  
FT NON\_TER 832  
SQ SEQUENCE 832 AA; 91899 MW; 173B830D6EF58A0C CRC64;

Query Match 45.0%; Score 49; DB 5; Length 832;  
Best Local Similarity 45.0%; Pred. No. 36;  
Matches 9; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 LRRASLGTCHAVRAIGRLSS 22  
||| |||||  
DB 657 IRRKWKTKGNATRALGRMAN 676

RESULT 10  
Q9V7G6 PRELIMINARY; PRT: 913 AA.  
ID Q9V7G6  
AC Q9V7G6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE MiCK protein.  
GN STPN-MiCK OR C08304 OR C018255.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;



```
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RI "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL: AL359716; CAD19433.1; -.
SQ SEQUENCE 541 AA; 59267 MW; 6825E62CF66E9B34 CRC64;

Query Match 44.0%; Score 48, DB 5, Length 541,
Best Local Similarity 54.5%; Pred. No. 37;
Matches 12; Conservative 3; Mismatches 3; Indels 4; Gaps 1;

QY 4 KRASLGIGHAVRAIG---RLS 21
   ||| ||||| |||
DB 28 RRSSTSGHADRLGDVAKRLS 49

RESULT 13
Q9N906 PRELIMINARY; PRI; 615 AA.
ID Q9N906
AC Q9N906;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Hypothetical 67.4 kDa protein.
GN L2464.09.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Brown S., Murphy L., Harris D., Ivens A.C., Quail M., Rajandream M.A.,
RA Barrell B.G.;
RI Submitted (JUL-2000) to the EMBL GenBank and DDBJ databases
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE 98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RI "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL: AL35154; CAB96741.1; -.
KW Hypothetical protein.
SQ SEQUENCE 615 AA; 67400 MW; A4AC2CCDB0F2DECB CRC64;

Query Match 44.0%; Score 48, DB 5, Length 615;
Best Local Similarity 54.5%; Pred. No. 37;
Matches 12; Conservative 3; Mismatches 3; Indels 4; Gaps 1;

QY 4 PRASLGIGHAVRAIG---RLS 21
   ||| ||||| |||
DB 102 RRSSTSGHADRLGDVAKRLS 123

RESULT 14
Q18906 PRELIMINARY; PRI; 133 AA.
ID Q18906
AC Q18906;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cysteine protease (Fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Phaditida; Phaditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN N2;
RX MEDLINE=96131081; PubMed 8525283;
RA Harrop S.A., Prociw P., Brindley P.J.;
RI "Amplification and characterization of cysteine proteinase genes from
RI nematodes.";
RL Trop. Med. Parasitol. 46:119-122(1995).
DR EMBL: L22447; AAB00354.1; -.
DR HSSP: P07688; IODO.
DR InterPro: IPR000668; Peptidase_C1.
DR InterPro: IPR000158; Peptidase_C1; 1.
DR Pfam: PF00112; Peptidase_C1; 1.
DR PRINTS: PRC0705; PAPAIN.
DR ProDom: PD000158; Peptidase_C1; 1.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
KW Protease.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 14247 MW; 3BC6FF593FCC17CB CRC64;

Query Match 43.1%; Score 47; DB 5; Length 133;
Best Local Similarity 59.2%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 ASLGIGHAVRAIG 18
   |||| ||||| ||
DB 105 ASLGGGHAVKMLG 117

RESULT 15
Q9P9N3 PRELIMINARY; PRI; 597 AA.
ID Q9P9N3
AC Q9P9N3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein X11587.
GN X11587 AND XF2762.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE 20365717; PubMed 10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abram F.A., Accencio M.,
RA Alvarado F., Alves L.M.C., Araya L.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA Colauto N.R., Colombo C., Costa F.P., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias Neto E., Dorena C., El-Dorfy H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA He P.L., Heheisel J.P., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.C.M., Lemos M.V.F., Lopes S.A., Lopes C.B., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.P., Marino C.L.,
RA Marques M.V., Martins D.A.L., Martins E.M.P., Matsukuma A.Y.,
RA Menck C.F.M., Miranda F.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Naqai M.A., Nascimento A.L.T.O., Netto L.F.S.,
RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto R.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,
RA Quaggio R.R., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.F., Silva W.A., Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Toranzo M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zata M., Meidanis J., Setubal J.C.;
RI "The genome sequence of the plant pathogen Xylella fastidiosa.";
RI Nature 406:151-159(2000).
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DR EMBL: AF003986; AAF84396.1;  
 DR EMBL: AF004682; AAF85547.1;  
 KW Hypothetical protein; complete protein.  
 SE SEQUENCE: 597 AA; 62491 MW; 94966.8673063E200 cRC64;

Query Match 43.1%; Score 41; DB 16; Length 597;  
 Best Local Similarity 66.7%; Field No. 52;  
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

27 6 AAGCTGCAVRAIDPL 20  
 14 3111111111  
 14 529 AAGG1BIVVSNIDPL 343

Search completed: January 2, 2003, 12:30:46.  
 Job time: 27.6 secs



